

OM of: US-09-801-115-2 to: EST: * out_format: pfs

Date: Jul 19, 2002 8:24 PM

About: Results were produced by the GenCore software, version 4.5.
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Command line parameters:

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-MODEL=frame+g2n.model -DEV=x1h
-o/cgcn2.1/USPTO_spool/US09801115/runat_19072002.182249_6105/app-query.fasta.1.156
-DB=EST -QPM=fastap -SUFFIX=first -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPTOL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YCAPOP=10.000 -YCAPEXT=0.500 -DELDP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blomsum2 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODAL=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500
-MINLEN=0 -MAXLEN=2000000000 -USER=US09801115 @CGN1.1.2376
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPRX -WAIT -THREADS=1
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Search information block:

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Query: US-09-801-115-2
Query Length: 99
Database: EST: *
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 1581.540000
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score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation
gb_est1:AA911088	-	508.00	1174.94	3.4e-56	386	AA911088 ok67e01.s1 NCI_CGAP_GC
gb_est1:AI989739	-	508.00	1174.81	3.4e-56	391	AI989739 wu21e10.x1 Soares_Died
gb_est1:AM183193	-	508.00	1174.68	3.5e-56	396	AM183193 xj6f11.x1 Soares_NFL
gb_est1:AA516431	-	508.00	1174.61	3.5e-56	399	AA516431 ne5a03.s1 NCI_CGAP_CC
gb_est1:AI989747	-	508.00	1174.53	3.6e-56	402	AI989747 wu21f09.x1 Soares_Died
gb_est1:AI982623	-	508.00	1174.36	3.6e-56	409	AI982623 wk35d10.x1 NCI_CGAP_PT
gb_est1:AI128804	-	508.00	1174.02	3.8e-56	423	AI128804 qa94b08.s1 Soares_fetd
gb_est1:AA455042	-	508.00	1173.93	3.8e-56	427	AA455042 aa04a07.s1 Soares_NHM
gb_est1:AA429945	-	508.00	1173.86	3.9e-56	432	AA429945 zw67f10.s1 Soares_test
gb_est1:AI078880	-	508.00	1173.36	4.1e-56	452	AI078880 cz37h05.x1 Soares_NHM
gb_est1:AI743235	-	508.00	1173.34	4.1e-56	453	AI743235 w99a02.x1 Soares_NSF
gb_est1:BF109912	-	508.00	1173.01	4.3e-56	468	BF109912 7117f03.x1 Soares_NSF
gb_est1:BF399486	-	508.00	1172.15	4.8e-56	514	BF399486 UI-R-CA1-bjb-b-12-0-01
gb_est1:BG05303	-	508.00	1171.69	5.1e-56	524	BG05303 602687808f1 NIH_MGC_95
gb_est1:BG031757	-	508.00	1171.88	5.1e-56	534	BG031757 602299819f1 NIH_MGC_87
gb_est1:BM472086	-	505.00	1165.59	1.1e-55	487	BM472086 AGEMCORRT_6469731 NIH
gb_est1:AA989129	-	504.00	1165.58	1.1e-55	386	AA989129 cr75h10.s1 NCI_CGAP_LD
gb_est1:BG529072	-	504.00	1158.52	2.8e-55	781	BG529072 602579169f1 NIH_MGC_60
gb_est1:BG249994	-	504.00	1156.44	3.6e-55	962	BG249994 602362062f1 NIH_MGC_90
gb_est1:BF691818	-	491.00	1132.01	8.3e-54	529	BF691818 60224787f1 NIH_MGC_62
gb_est1:BG613984	-	484.00	1117.41	5.4e-53	443	BG613984 602641513f1 NIH_MGC_61
gb_est1:AV759888	-	480.00	1108.30	1.7e-52	432	AV759888 AV759888 MDS Homo sapi
gb_est1:AI141284	-	476.50	1101.01	4.4e-52	393	AI141284 qa52h10.s1 Soares_NHM
gb_est1:AI265924	-	475.00	1098.92	6.0e-52	353	AI265924 qx66d08.x1 NCI_CGAP_OY
gb_est1:BF203359	-	475.00	1088.92	2.1e-51	930	BF203359 60186568f1 NIH_MGC_17
gb_est1:W52820	-	472.00	1088.78	2.1e-51	468	W52820 zc55c06.f1 Soares_seneso
gb_est1:AA876539	-	471.50	1086.42	2.9e-51	551	AA876539 oca4h08.s1 NCI_CGAP_PT
gb_est1:AA702011	-	471.50	1085.98	3.0e-51	551	AA702011 z17f0d02.s1 Soares_fetd
gb_est1:AF151058	-	471.50	1083.39	4.1e-51	692	AF151058 Homo sapiens HSPC224 p
gb_est1:AV683453	-	471.50	1082.55	4.7e-51	776	AV683453 AV683453 GKC Homo sapi
gb_est1:N89912	-	471.00	1087.79	2.4e-51	409	N89912 zb22g09.s1 Soares_fetal
gb_est1:BF37159	-	467.50	1073.02	1.6e-50	789	BF37159 601305091f1 NIH_MGC_39
gb_est1:BG532587	-	463.00	1068.23	3.8e-50	678	BG532587 602562152f1 NIH_MGC_61
gb_est1:BT561562	-	460.50	1058.16	1.1e-49	678	BT561562 60356562f1 NIH_MGC_97
gb_est1:AA887264	-	453.00	1045.39	5.3e-49	333	AA887264 os11a06.s1 NCI_CGAP_LD
gb_est1:AI633679	-	445.50	1026.11	6.6e-48	500	AI633679 lh71c04.x1 Soares_NHM
gb_est1:BF917173	-	445.50	1023.42	9.3e-48	654	BF917173 602515173f1 NIH_MGC_84
gb_est1:AI633661	-	444.00	1026.89	6.0e-48	326	AI633661 qp62b12.x1 Soares_fetd
gb_est1:W93646	-	442.50	1017.17	2.1e-47	606	W93646 zq97d08.s1 Soares_fetd
gb_est1:BB875161	-	433.00	1004.81	1.0e-46	456	BB875161 60188641f1 NIH_MGC_69

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gb_est1:AI349474 - 435.00 1006.05 8.6e-47 319 ! AI349474 qp22f07.x1 Soares_f
gb_est1:AI371387 - 435.00 1005.86 8.8e-47 325 ! AI371387 qo84b02.x1 NCI_CGAP
gb_est1:AA305052 + 433.00 999.38 2.0e-46 389 ! AA305052 EST176055 Colon car
gb_est1:AV754613 - 430.50 990.38 6.4e-46 533 ! AV754613 AV754613 TP Homo sa
gb_est1:BF388158 - 420.00 970.58 8.2e-45 331 ! BF388158 UI-R-CA1-bby-h-12-0
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seq_name: gb_est1:AA911088

seq_documentation_block:

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LOCUS AA911088 386 bp mRNA linear EST 09-JUN-1998
DEFINITION ok67e01.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1519032 3',
RNA sequence.
ACCESSION AA911088.1 GI:3050378
VERSION EST.
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
```

REFERENCE

1 (bases 1 to 386)

AUTHORS

NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgapdb@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.lnl.gov/bdrrp/image/image.html
Insert Length: 381 Std Error: 0.00
Seq primer: -40m13 fwd. ER from Amersham
High quality sequence stop: 79.

FEATURES

Location/Qualifiers

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1..386
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1519032"
/clone_lib="NCI_CGAP_GC4"
/tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
/notes="vector: pTR73D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from 3 pooled
germ cell tumors, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pTR73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."
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BASE COUNT

113 a 87 c 81 g 105 t

alignment_scores:

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Quality: 508.00 Length: 99
Ratio: 5.131 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000
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alignment_block:

US-09-801-115-2 x AA911088/rev ..
Align seg 1/1 to reverse of: AA911088 from: 1 to: 386

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1 MetaspasValGlnProlystlelySHsArgProphesysheserA 17
|||||
357 ATGATTAACCTGACGCGAATAAACACGCCCTTCCTGCTGAGTGT 308
|||||
17 TTGAGTAAATGATGATGATGATGATGATGATGATGATGATGAT 34
|||||
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307 GAAAGCCAGCTGAAGATGCTGCGCTGGATATATATCACTGCTGTAA 258
 34 hrThrvAlpHemleuileValserVallleuAlaleuileProgluThr 50
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 257 CAACGATATTCATGCTCATGCTATCTGTGGACGATGATACCAAGAAC 208
 51 ThrThrvleuThrValGlyGlyValAlpheAlaleuValThrAlaValCy 67
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 207 ACAACATTTGACAGTTGGTGGAGGGGTGTTGCACTGTGACAGCATATG 158
 67 scYsleuAlaAspGlyAlaLeuileTyArGlylsleuLeuPheAsnPro 84
 |||||||
 157 CTGCTTCCCGACGGGGCCCTTATTATCCGAGACTTCTGTGCATATCCA 108
 84 erglYProTyrGlnLysLysProValHISgluLysgluValleu 99
 |||||||
 107 GCGGCTCTTACCAAGAAAGCCTGTGCATGAAAAAAGAGTTTGG 61

seq_name: gb_est1:AI989739

seq_documentation_block:

LOCUS AI989739 391 bp mRNA linear EST 27-OCT-1999
 DEFINITION wu21e10.x1 Soares_Dieckgraefe_colon_NHCD Homo sapiens cDNA clone
 IMAGE:2520714 3', mRNA sequence.

ACCESSION AI989739

VERSION AI989739.1 GI:5836620

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 391)

REFERENCE NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.jnl.gov) for further information.
 Seq primer: -400P from Gibco.

FEATURES
 Location/Qualifiers

1..391

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2520714"

/clone_lib="Soares_Dieckgraefe_colon_NHCD"

/tissue_type="colonic mucosa from 3 patients with Crohn's
 disease"

/lab_host="DH10B (phage-resistant)"

/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
 modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
 strand cDNA was primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGGCGCGCTTTTCTTTTCTTTT 3'],
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization. Tissue samples
 provided by Dr. Brian Dieckgraefe (Washington University,
 dieckelm.wustl.edu); colonic mucosa represents a range of
 disease involvement from moderate to severe Crohn's
 disease; samples include both perforating (fistulas) and
 non-perforating samples. Library constructed by Bento
 Soares and M. Fatima Bonaldo.

BASE COUNT 113 a 90 c 81 g 107 t
 ORIGIN

alignment_scores:

Quality: 508.00 Length: 99
 Ratio: 5.131 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-801-115-2 x AI989739/rev ..
 Align seg 1/1 to reverse of: AI989739 from: 1 to: 391

1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVal 17
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 358 ATGGATTAACGTGCAGCCGCAAAATTAACATCGCCCTTCTGCTCAGTGT 309
 17 llysglYHISValLysMetLeuArgLeuAspIleLeuSnsrLeuValT 34
 |||||||
 308 GAAAGCCAGCTGAAGATGCTGCGCTGGATATATCACTGCTGTAA 259
 34 hrThrvAlpHemleuileValserVallleuAlaleuileProgluThr 50
 |||||||
 258 CAACGATATTCATGCTCATGCTATCTGTGGACGATGATACCAAGAAC 209
 51 ThrThrvleuThrValGlyGlyValAlpheAlaleuValThrAlaValCy 67
 |||||||
 208 ACAACATTTGACAGTTGGTGGAGGGGTGTTGCACTGTGACAGCATATG 159
 67 scYsleuAlaAspGlyAlaLeuileTyArGlylsleuLeuPheAsnPro 84
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 158 CTGCTTCCCGACGGGGCCCTTATTATCCGAGACTTCTGTGCATATCCA 109
 84 erglYProTyrGlnLysLysProValHISgluLysgluValleu 99
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 108 GCGGCTCTTACCAAGAAAGCCTGTGCATGAAAAAAGAGTTTGG 62

seq_name: gb_est1:AM183193

seq_documentation_block:

LOCUS AM183193 396 bp mRNA linear EST 18-NOV-1999
 DEFINITION x167f11.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
 IMAGE:2662317 3', mRNA sequence.

ACCESSION AM183193

VERSION AM183193.1 GI:6451679

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 396)

REFERENCE NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov

This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.jnl.gov) for further information.
 Seq primer: -400P from Gibco.

FEATURES
 Location/Qualifiers

1..396

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2662317"

/clone_lib="Soares_NFL_T_GBC_S1"

/lab_host="DH10B"

/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from three normalized
 libraries (fetal lung NBH119W, testis NHT, and B-cell
 NCI-CCGAP GCB1) were mixed, and ss circles were made in
 vitro. Following HAP purification, this DNA was used as
 tracer in a subtractive hybridization reaction. The driver
 was PCR-amplified cDNAs from pools of 5,000 clones made
 from the same 3 libraries. The pools consisted of
 1 M.A.G.E. clones 297480-302087, 682632-687239,
 726408-728711, and 729096-731399. Subtraction by Bento
 Soares and M. Fatima Bonaldo.

BASE COUNT 115 a 92 c 80 g 109 t
 ORIGIN

alignment_scores:
Quality: 508.00 Length: 99
Ratio: 5.131 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-801-115-2 x AW183193/rev ..

Align seg 1/1 to reverse of: AW183193 from: 1 to: 396

1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerVa 17
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17 LysGlyHisValLysMetLeuArgLeuAspIleLeuSerLeuValT 34
|||||
309 GAAGGCCGCGTGAAGATGCTGCGGCTGATATATCACTACACTGCTGTA 260
34 hrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
|||||
259 CAACAGTATCATGCTCATCTCTGTTGGCAGCATGATACCGAAGAAC 210
51 ThrThrLeuThrValGlyGlyValAlaPheAlaLeuValThrAlaValCy 67
|||||
209 ACAACATTGACAGTGTGGAGGGGTGTTGCACCTGTGACACAGATATG 160
67 scLysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProS 84
|||||
159 CTGCTCTCCGACGCGGCGCTTATTTACCGAGCTTCTGTTCATGCCA 110
84 ergLysProTyrGlnLysLysProValHisGluLysLysGluValLeu 99
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109 GCGGTCTTACCAGAAAAGCCTGTGCATGAAGAAAGAGTTTGG 63

seq_name: gb_estl:AA516431

seq_documentation_block:
LOCUS AA516431 399 bp mRNA linear EST 13-AUG-1997
DEFINITION ne58a03.s1 NCI_CGAP_C03 Homo sapiens CDNA clone IMAGE:901516 3',
mRNA sequence.
ACCESSION AA516431
VERSION AA516431.1 GI:2255955
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 399)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.lnl.gov/bdrp/image/image.html
Insert Length: 527 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham.

FEATURES
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1..399
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="901516"
/clone_idb="NCI_CGAP_C03"
/sex="pooled"

/tissue_type="colon"
/lab_host="DH10B"
/note="vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from 12 pooled bulk tumor samples and primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library went through one round of
normalization."

BASE COUNT 115 a 94 c 81 g 109 t
ORIGIN

alignment_scores:
Quality: 508.00 Length: 99
Ratio: 5.131 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-801-115-2 x AA516431/rev ..

Align seg 1/1 to reverse of: AA516431 from: 1 to: 399

1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerVa 17
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357 ATGGATTAACGTCGACGCGAAATATAACATCGCCCTTCTGCTTCAGTGT 308
17 LysGlyHisValLysMetLeuArgLeuAspIleLeuSerLeuValT 34
|||||
307 GAAGGCCGCGTGAAGATGCTGCGGCTGATATATCACTACACTGCTGTA 258
34 hrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
|||||
257 CAACAGTATCATGCTCATCTCTGTTGGCAGCATGATACCGAAGAAC 208
51 ThrThrLeuThrValGlyGlyValAlaPheAlaLeuValThrAlaValCy 67
|||||
207 ACAACATTGACAGTGTGGAGGGGTGTTGCACCTGTGACACAGATATG 158
67 scLysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProS 84
|||||
157 CTGCTCTCCGACGCGGCGCTTATTTACCGAGCTTCTGTTCATGCCA 108
84 ergLysProTyrGlnLysLysProValHisGluLysLysGluValLeu 99
|||||
107 GCGGTCTTACCAGAAAAGCCTGTGCATGAAGAAAGAGTTTGG 61

seq_name: gb_estl:AI989747

seq_documentation_block:
LOCUS AI989747 402 bp mRNA linear EST 27-OCT-1999
DEFINITION wu21f09.x1 Soares-Dieckgraefe_colon_NHCD Homo sapiens CDNA clone
IMAGE:2520713 3', mRNA sequence.
ACCESSION AI989747
VERSION AI989747.1 GI:5836628
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 402)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
CONTACT: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LINL; contact the
IMAGE Consortium ([info@image.lnl.gov](http://info/image.lnl.gov)) for further information.
Seq primer: -40up from Gibco.

FEATURES
source
1..402
Location/Qualifiers


```

seq.documentation_block:
LOCUS      A1128804               423 bp      mRNA      linear      EST 05-OCT-1998
DEFINITION g94b08.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
IMAGE:1694391 3', mRNA sequence.
ACCESSION  A1128804
VERSION    A1128804
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 423)
AUTHORS   NC-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL   Unpublished (1997)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgaps@email.nih.gov
            This clone is available royalty-free through LNLN; contact the
            IMAGE Consortium (info@image.lnl.gov) for further information.
            Insert Length: 382 Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 413.
FEATURES
    source
        1..423
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone_lib="Soares_fetal_heart_NbHH19W"
        /sex="unknown"
        /dev_stage="19 weeks"
        /lab_host="DH10B (ampicillin resistant)"
        /note="Organ: heart; Vector: p773D (Pharmacia) with a
        modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
        strand cDNA was primed with a Not I - oligo(dT) primer [5'
        TGTTCACATCGAAGTGGAGCGGCGCATCTTTTCTTTTCTTTT 3']
        double-stranded cDNA was size selected, ligated to Eco RI
        adapters (Pharmacia), digested with Not I and cloned into
        (Pharmacia). Library went through one round of
        normalization to a Cot = 5. Library constructed by
        M.Fatima Bonaldo. This library was constructed from the
        same fetus as the fetal lung library, Soares fetal lung
        NBHL19W."
BASE COUNT      116 a      101 c      89 g      117 t
ORIGIN
alignment_scores:
    Quality: 508.00      Length: 99
    Ratio: 5.131      Gaps: 0
    Percent Similarity: 100.000      Percent Identity: 100.000
alignment_block:
US-09-801-115-2 x A1128804/rev ..
Align seg 1/1 to reverse of: A1128804 from: 1 to: 423
1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerVal 17
333 ATGGATACGGCGACCGCAAAATTAACATCGCCCCCTTCTGCTTCAGTGT 304
17 llysglyhlyvalysmetleuargleuaspllelleasnsleuValt 34
303 GAAAGCGCCACGCGAGATGCTGGCGCGATATTTCAACTACATCGTAA 254
34 hrtThValPheMetleuIleValSerValIleAlaIleuIleProGluThr 50
253 CAACAGTATTCATGCTCATGCTATCTGTGTGGCAGTATGACCAAGAAC 204
51 ThrThrleuThValGlyGlyValPheAlaIleuValIThrAlaValCyl 67
203 ACAACATTCACAGTTGTGTGGAGGGGTGTTTGCACCTTGACAGCAGTATG 154

```

```

seq_name: gb_est1:AA455042
seq.documentation_block:
LOCUS      AA455042               427 bp      mRNA      linear      EST 06-JUN-1997
DEFINITION aa04a07.s1 Soares_NbHMPu_S1 Homo sapiens cDNA clone IMAGE:812244
3', mRNA sequence.
ACCESSION  AA455042
VERSION    AA455042.1 GI:2177818
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 427)
AUTHORS   Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
            Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
            Scheinberg, K., Stepien, M., Tan, F., Theisling, B., White, T., Wylie
            T., Waterston, R., and Wilson, R.
JOURNAL   Unpublished (1997)
COMMENT   Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LNLN; contact the
            IMAGE Consortium (info@image.lnl.gov) for further information.
            Seq primer: -41m13 fwd. ET from Amersham
            High quality sequence stop: 395.
FEATURES
    source
        1..427
        /organism="Homo sapiens"
        /db_xref="GDB:6043155"
        /db_xref="taxon:9606"
        /clone_lib="Soares_NbHMPu_S1"
        /clone_image="812244"
        /tissue_type="Pooled human melanocyte, fetal heart, and
        pregnant uterus"
        /lab_host="DH10B"
        /note="Organ: mixed (see below); Vector: p773D-Pac
        (Pharmacia) with a modified polylinker; Site_1: Not I;
        Site_2: Eco RI; Equal amounts of plasmid DNA from three
        normalized libraries (melanocyte 2NBH, pregnant uterus
        NBHPU, and fetal heart NBHH19W) were mixed, and ss circles
        were made in vitro. Following HAP purification, this DNA
        was used as tracer in a subtractive hybridization
        reaction. The driver was PCR-amplified cDNAs from pools of
        5,000 clones made from the same 3 libraries. The pools
        consisted of I.M.A.G.E. clones 260232-265223,
        340488-345479, and 484488-489479."
BASE COUNT      119 a      101 c      91 g      116 t
ORIGIN
alignment_scores:
    Quality: 508.00      Length: 99
    Ratio: 5.131      Gaps: 0
    Percent Similarity: 100.000      Percent Identity: 100.000
alignment_block:
US-09-801-115-2 x AA455042/rev ..
Align seg 1/1 to reverse of: AA455042 from: 1 to: 427

```

1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerVa 17
 356 ATGCATACGTCGACGCCGAAATAAACATCGCCCTTCTGCTTCACTGT 307
 17 LlysgLysHisValLysMetLeuArgLeuAspIleIleAsnSerLeuValT 34
 306 GAAGGCCACGTCGAGATGTCGCGGATATATATCACTGACTGTGTA 257
 34 hThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
 256 CAACAGATTATGCTCATCTGATCTGTGTCGACGATGACGGAAC 207
 51 ThrThrLeuThrValGlyGlyValAlaPheAlaLeuValThrAlaValCy 67
 206 ACAACATTGACAGTTGGTGGAGGGGTTTGCACCTGTCGACGACGATG 157
 67 sCysLeuAlaAspGlyAlaLeuIleTyArgLysLeuLeuPheAsnProS 84
 156 CTGCTTGGCCGACGGGCCCTTATTACCGGAACCTTCTGTCAATCCA 107
 84 ergLysProTyGlnLysLysProValHisGluLysLysGluValLeu 99
 106 GCGGCTCTTACCAAGAAAGCCCTGTCATGATAAAAGAAAGTTTGG 60

seq_name: gb_est1:AA429945

seq_documentation_block:

LOCUS AA429945 432 bp mRNA linear EST 16-OCT-1997
 DEFINITION 2w67f10.s1 Soares testis_NHT Homo sapiens cDNA clone IMAGE:781291

ACCESSION AA429945
 VERSION AA429945.1 GI:2113244

KEYWORDS 3' mRNA sequence.
 EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 432)
 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisler, G., Jost, S.,
 Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B.,
 Schellenberg, K., Stepien, M., Tan, F., Theisling, B., White, Y., Wyllie,
 T., Waterston, R. and Wilson, R.
 Masnu-Merck EST Project 1997

TITLE JOURNAL
 COMMENT Unpublished (1997)
 Contact: Wilson RK
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.edu

FEATURES
 Source
 High quality sequence stop: 421.

1.432
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:781291"
 /clone_lib="Soares_testis_NHT"
 /sex="male"
 /lab_host="DH10B"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
 was prepared from mRNA obtained from Clontech Laboratories
 , Inc. and primed with a Not I - oligo(dT) primer [5'
 TGTACCAATCTGAAGTGGAGCGGCCCAATTTTCTTTTCTTTT 3']
 (Pharmacia), digested with Not I and cloned into the Not I
 and Eco RI sites of the modified pT73 vector. Library
 went through one round of normalization to Cots, and was
 constructed by Bento Soares and W. Fatima Bonaldo."

BASE COUNT 119 a 101 c 92 g 120 t
 ORIGIN

alignment_scores:
 Quality: 508.00 Length: 99
 Ratio: 5.131 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment block:
 US-09-801-115-2 x AA429945/rev ..

Align seg 1/1 to reverse of: AA429945 from: 1 to: 432

1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerVa 17
 361 ATGCATACGTCGACGCCGAAATAAACATCGCCCTTCTGCTTCACTGT 312
 17 LlysgLysHisValLysMetLeuArgLeuAspIleIleAsnSerLeuValT 34
 311 GAAGGCCACGTCGAGATGTCGCGGATATATATCACTGACTGTGTA 262
 34 hThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
 261 CAACAGATTATGCTCATCTGATCTGTGTCGACGATGACGGAAC 212
 51 ThrThrLeuThrValGlyGlyValAlaPheAlaLeuValThrAlaValCy 67
 211 ACAACATTGACAGTTGGTGGAGGGGTTTGCACCTGTCGACGACGATG 162
 67 sCysLeuAlaAspGlyAlaLeuIleTyArgLysLeuLeuPheAsnProS 84
 161 CTGCTTGGCCGACGGGCCCTTATTACCGGAACCTTCTGTCAATCCA 112
 84 ergLysProTyGlnLysLysProValHisGluLysLysGluValLeu 99
 111 GCGGCTCTTACCAAGAAAGCCCTGTCATGATAAAAGAAAGTTTGG 65

seq_name: gb_est1:A1078580

seq_documentation_block:

LOCUS A1078580 452 bp mRNA linear EST 10-AUG-1998
 DEFINITION 0537H05.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1677561

ACCESSION A1078580
 VERSION A1078580.1 GI:3412988

KEYWORDS 3' mRNA sequence.
 EST.

SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 452)
 NCBI-CCG http://www.ncbi.nlm.nih.gov/ncicgdp.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: ccgaps-r@emil.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Seq primer: -40m13 fwd. ET from Amersham

FEATURES
 source
 High quality sequence stop: 410.

1.452
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1677561"
 /clone_lib="Soares_NhHMPu_S1"
 /tissue_type="Pooled human melanocyte, fetal heart, and
 pregnant uterus"
 /lab_host="DH10B"
 /note="Organ: mixed (see below); Vector: pT73D-Pac
 (Pharmacia) with a modified polylinker; site_1: Not I;

Site 2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NDH, pregnant uterus NBHPV, and fetal heart NBH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 26032-26523, 34048-34547, and 48488-48947.

BASE COUNT 125 a 110 c 97 g 120 t
ORIGIN

alignment_scores:

Quality: 508.00 Length: 99
Ratio: 5.131 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-801-115-2 x A1078580/rev ..

Align seg 1/1 to reverse of: A1078580 from: 1 to: 452

```

1 MetaspasnaValGlnProLysIleLysHisArgProphecysPheSerVa 17
|||||
359 ATGGATTAACGTCGACGCCGAAATATAACATCGCCCTTCTGCTTCACTGT 310
17 LysGlyHisValLysMetLeuArgLeuAspIleIleAsnSerLeuValT 34
|||||
309 GAAAGGCCACGTGAAGATGCGCGCTGATATATCACTCACTCACTGTAA 260
34 hTrhValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
|||||
259 CAACAGTATTCATCTCATCTATCTGTGTGGCATGATACCAAGAAC 210
51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCy 67
|||||
209 ACAACATTAACAGTTGGTGGAGGGCTTTGCACTTGTGACAGCATATG 160
67 sCyLeuAlaAspGlyAlaLeuIleIleTyrArgLysLeuLeuPheAsnPro 84
|||||
159 CTGCTTCCTTACCGAAGAACCTGTATTTACCGAAGCTTCTGTCAATCCCA 110
84 eArgLysProTyrGlnLysLysProValHisGluLysGluValLeu 99
|||||
109 GCGGCTCTTACCGAAGAACCTGTATTTACCGAAGAACCTTTTG 63

```

seq_name: gb_est1:A1743235

seq_documentation_block:

LOCUS A1743235 453 bp mRNA linear EST 20-DEC-1999
DEFINITION Wg90a02.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3372330 3', mRNA sequence.

ACCESSION A1743235
VERSION A1743235.1 GI:5111523

KEYWORDS

EST.
human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE 1 (bases 1 to 453)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 378 Std Error: 0.00
Seq primer: -400p from Gibco.

FEATURES

source 1..453
Location/Qualifiers

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2372330"
/clone_id="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152337 Soares NB2HR8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306511, 320136-322823, 326280-32663 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."

alignment_scores:

Quality: 508.00 Length: 99
Ratio: 5.131 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-801-115-2 x A1743235/rev ..

Align seg 1/1 to reverse of: A1743235 from: 1 to: 453

```

1 MetaspasnaValGlnProLysIleLysHisArgProphecysPheSerVa 17
|||||
362 ATGGATTAACGTCGACGCCGAAATATAACATCGCCCTTCTGCTTCACTGT 313
17 LysGlyHisValLysMetLeuArgLeuAspIleIleAsnSerLeuValT 34
|||||
312 GAAAGGCCACGTGAAGATGCGCGCTGATATATCACTCACTCACTGTAA 263
34 hTrhValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
|||||
262 CAACAGTATTCATCTCATCTATCTGTGTGGCATGATACCAAGAAC 213
51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCy 67
|||||
212 ACAACATTAACAGTTGGTGGAGGGCTTTGCACTTGTGACAGCATATG 163
67 sCyLeuAlaAspGlyAlaLeuIleIleTyrArgLysLeuLeuPheAsnPro 84
|||||
162 CTGCTTCCTTACCGAAGAACCTGTATTTACCGAAGCTTCTGTCAATCCCA 113
84 eArgLysProTyrGlnLysLysProValHisGluLysGluValLeu 99
|||||
112 GCGGCTCTTACCGAAGAACCTGTATTTACCGAAGAACCTTTTG 66

```

seq_name: gb_est2:BF109912

seq_documentation_block:

LOCUS BF109912 468 bp mRNA linear EST 20-OCT-2000
DEFINITION 717103.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:3526805 3' similar to TR:090141 090141 CHROMKINE-LIKE FACTOR
1. [1] ; mRNA sequence.

ACCESSION BF109912
VERSION BF109912.1 GI:10939602

KEYWORDS

EST.
human.

ORGANISM

Homo sapiens

REFERENCE

AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE 1 (bases 1 to 468)
JOURNAL NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 378 Std Error: 0.00
Seq primer: -400p from Gibco.

FEATURES

source 1..468
Location/Qualifiers

REFERENCE 1 (bases 1 to 468)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 JOURNAL Tumor Gene Index
 COMMENT Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: 400p from G1bco.
 FEATURES
 source
 1. 468
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:3526805"
 /clone_1lb="Soares_NSF_F8_9W_OT_PA_P_S1"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
 a modified polylinker; Site_1: Not I; Site_2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.
 Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 PCR-amplified cDNAs from pools of 5,000 clones made from
 the same 5 libraries. The pools consisted of the following
 libraries and clones: Soares NBHF pool 1:
 309384-310919, 323208-325895 Soares NB2HP pool 1:
 145032-147335, 147720-148103, 148872-149255, 15002 -
 150407, 151176-153327 Soares NB2HR8-9W pool 1:
 758280-760583, 772104-774407 Soares NBHPA pool 1:
 304776-306311, 320136-322823, 326280-32663 Soares NBHOT
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT 127 a 116 c 102 g 123 t
 ORIGIN

alignment_scores:
 Quality: 508.00 Length: 99
 Ratio: 5.131 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-801-115-2 x BF109912/rev ..

Align seg 1/1 to reverse of: BF109912 from: 1 to: 468

```

1 MetaspasnaValGlnProLysIleLysHisArgProPheserVa 17
|||||
362 ATGATTAACGTCGACCGGAAATAAACATCGCCCTTCGCTCACTGT 313
|||||
17 LlysGlyHisValLysMetLeuArgLeuAspIleIleAsnSerLeuValT 34
|||||
312 GAAAGGCCACGCTGAGATGCTCGCGCTGATATTATCACTACCTGTTAA 263
|||||
34 htrhrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
|||||
262 CAACAGATTTCATGCTCATGTCATCTGTGGCAGCATGATACCGAAGACC 213
|||||
51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCy 67
|||||
212 ACAACATTGACAGTTGGTGAGGGGTGTTGCACTGTGACAGCAGATATG 163
|||||
67 scysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnPro 84
|||||
162 CTGCTTGGCCGACGGGCCCTTATTATCCGGAACCTTCGTTCAATCCA 113
|||||
84 ergGlyProTyrGlnLysLysProValHisGlyLysGluValLeu 99
|||||
112 GCGGCTCTTACCAAGAAAGCGCTGTGCATGAAGAAAGAGTTTGG 66
|||||
seq_name: gb_est2:BF399486
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seq_documentation_block:

LOCUS BF399486 510 bp mRNA linear EST 27-NOV-2000
 DEFINITION UI-R-CAI-bjb-b-12-0-UI-s1 UI-R-CAI Rattus norvegicus cDNA clone
 UI-R-CAI-bjb-b-12-0-UI 3', mRNA sequence.
 ACCESSION BF399486
 VERSION BF399486.1 GI:11384494
 KEYWORDS EST.
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE 1 (bases 1 to 510)
 AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
 TITLE Normalization and subtraction: two approaches to facilitate gene
 JOURNAL Genome Res. 6 (9), 791-806 (1996)
 MEDLINE 97044477
 COMMENT Contact: Soares, MB
 Program for Rat Gene Discovery and Mapping
 University of Iowa
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA
 Tel.: 319 335 8250
 Fax: 319 335 9365
 Email: msoares@blue.weeg.uiowa.edu
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first
 strand cDNA and therefore this may represent a bonafide poly A
 tail. cDNA library Preparation: M.B. Soares lab Clone distribution:
 clones will be available through Research Genetics (www.resgen.com)
 Seq primer: M13 Forward
 POLYA=Yes..

FEATURES
 source
 1. 510
 Location/Qualifiers
 /organism="Rattus norvegicus"
 /strain="Sprague-Dawley"
 /db_xref="taxon:10116"
 /clone="UI-R-CAI-bjb-b-12-0-UI"
 /clone_1lb="UI-R-CAI"
 /lab_host="DH10B (Life Technologies)"
 /note="Vector: pT73D-Pac (Pharmacia) with a modified
 polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAI
 library is a subtracted library derived from the following
 tissues: thalamus, cerebellum, hypothalamus, medulla, pons
 hippocampus. For a detailed description of the library
 from which this clone was derived, please visit our web
 site at ratest.eng.uiowa.edu. The subtraction has been
 previously described in (Bonaldo, Lennon and Soares,
 Genome Research 6:791-806, 1996)
 TAG_SEQ=None found"

BASE COUNT 130 a 131 c 104 g 145 t
 ORIGIN

alignment_scores:
 Quality: 508.00 Length: 99
 Ratio: 5.131 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-801-115-2 x BF399486/rev ..

Align seg 1/1 to reverse of: BF399486 from: 1 to: 510

```

1 MetaspasnaValGlnProLysIleLysHisArgProPheserVa 17
|||||
371 ATGGATTAACGTCGACCGGAAATAAACATCGCCCTTCGTTAAGTGT 322
|||||
17 LlysGlyHisValLysMetLeuArgLeuAspIleIleAsnSerLeuValT 34
|||||
321 GAAAGGCCACGCTGAGATGCTCGCGCTGATATTATCAACTACTGTTAA 272
|||||
```


34 hrThrValPheMetLeuIleValSerValIleuAlaLeuIleProGluThr 50
 |||||||
 271 CAACAGTATTCATGCTCATCGTATCTGTGTGGCAGTATCCAGCAAAAC 222
 51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCly 67
 |||||||
 221 ACAACATTGACAGTGTGGAGGGGTGTTCACACTGTGGACAGCAGTATG 172
 67 sCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnPro 84
 |||||||
 171 CTGCTCTCCGCGCGGGCCCTTATTACCGGAGCTCTGTTCATCCCA 122
 84 exGlyProTyrGlnLysLysProValHisGlyLysGlyValLeu 99
 |||||||
 121 GCGGTCCTTACAGAAAAAGCCTGTGATGAAGAAAAAGAGTTTGG 75

seq_name: gb_est2:BG705303

seq_documentation_block:

LOCUS BG705303 524 bp mRNA linear EST 07-MAY-2001
 DEFINITION 602687808F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4820568 5',
 mRNA sequence.
 ACCESSION BG705303
 VERSION BG705303.1 GI:13979504
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 524)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM10725 row: 0 column: 01
 High quality sequence stop: 521.

FEATURES
 source
 1..524
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4820568"
 /clone_lib="NIH_MGC_95"
 /tissue_type="hippocampus"
 /lab_host="DH10B"
 /note="Organ: Brain; Vector: pBluescript (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcagag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',
 size-selected for average insert size 2.5 kb and
 normalized to R0F 5. This is a primary library enriched
 for full-length clones and constructed using the
 cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."

BASE COUNT 142 a 113 c 138 g 131 t
 ORIGIN

alignment_scores:
 Quality: 508.00 Length: 99
 Ratio: 5.131 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-801-115-2 x BG705303

Align seq 1/1 to: BG705303 from: 1 to: 524

1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVa 17
 |||||||
 141 ATGCATTAACGTGCACGCCGAAATTAACATCGCCCTCTGCTTCAGTGT 190
 17 LysGlyHisValLysMetLeuArgLeuAspIleIleAsnSerLeuVal 34
 |||||||
 191 GAAAGGCCACGTGAAGATGCTGGGGCTGGATATTATCAACTCAGTGTA 240
 34 hrThrValPheMetLeuIleValSerValIleuAlaLeuIleProGluThr 50
 |||||||
 241 CAACAGTATTCATGCTCATGCTGTGTGGCAGTATCCAGCAAAAC 290
 51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCly 67
 |||||||
 291 ACAACATTGACAGTGTGGAGGGGTGTTCACCTGTGTGACAGCAGTATG 340
 67 sCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnPro 84
 |||||||
 341 CTGCTCTCCGCGCGGGCCCTTATTACCGGAGCTCTGTTCATCCCA 390
 84 exGlyProTyrGlnLysLysProValHisGlyLysGlyValLeu 99
 |||||||
 391 GCGGTCCTTACAGAAAAAGCCTGTGATGAAGAAAAAGAGTTTGG 437

seq_name: gb_est2:BG031757

seq_documentation_block:

LOCUS BG031757 534 bp mRNA linear EST 24-JAN-2001
 DEFINITION 602298619F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4394093 5',
 mRNA sequence.
 ACCESSION BG031757
 VERSION BG031757.1 GI:12422364
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 534)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LLM10089 row: e column: 06
 High quality sequence stop: 446.

FEATURES
 source
 1..534
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4394093"
 /clone_lib="NIH_MGC_87"
 /tissue_type="mammary adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: breast; Vector: PCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: this is a NIH_MGC Library."

BASE COUNT 163 a 108 c 132 g 131 t
 ORIGIN

alignment_scores:

Quality: 508.00 Length: 99
Ratio: 5.131 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-801-115-2 x BG031757 ..

Align seg 1/1 to: BG031757 from: 1 to: 534

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1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVa 17
|||||
123 ATGGATTACGTCGACGCCGAAATATAAACATCGCCCTTCTGCTTCAGTGT 172
17 LysGlyHisValLysMetLeuArgLeuAspIleIleAsnSerLeuValP 34
|||||
173 GAAAGGCCACGTGAAGATGCTGGGGCTGGATATTATCACTCACTGGTAA 222
34 hrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
|||||
223 CAACAGTATTCATGCTCATGCTATCTGTGGCAGCTGATACCGAAGACC 272
51 ThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAlaValCy 67
|||||
273 ACAACATTGACAGTGGTGGAGGGGGTGTTCACCTGTGTGACAGCAGTATG 322
67 sCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProS 84
|||||
323 CTGCTTGGCCGACGGGCCCTTATTATCCGGAAGCTTCTCTCATGCCA 372
84 ergLysProTyrGlnLysLysProValHisGluLysLysGluValLeu 99
|||||
373 GCGGTCTTACCAAGAAAAAGCCTGTGCATGAAAAAAGAAAGATTGTG 419
```


[illegible]

PR 23-MAY-1997; 97US-0047613.
 PR 23-MAY-1997; 97US-0047614.
 PR 23-MAY-1997; 97US-0047615.
 PR 23-MAY-1997; 97US-0047617.
 PR 23-MAY-1997; 97US-0047618.
 PR 23-MAY-1997; 97US-0047632.
 PR 23-MAY-1997; 97US-0047633.
 PR 06-JUN-1997; 97US-0048964.
 PR 06-JUN-1997; 97US-0048964.
 PR 13-JUN-1997; 97US-0049610.
 PR 08-JUL-1997; 97US-0051926.
 PR 16-JUL-1997; 97US-0052874.
 PR 18-AUG-1997; 97US-0055724.
 PR 22-AUG-1997; 97US-0056630.
 PR 22-AUG-1997; 97US-0056631.
 PR 22-AUG-1997; 97US-0056632.
 PR 22-AUG-1997; 97US-0056636.
 PR 22-AUG-1997; 97US-0056637.
 PR 22-AUG-1997; 97US-0056662.
 PR 22-AUG-1997; 97US-0056664.
 PR 22-AUG-1997; 97US-0056845.
 PR 22-AUG-1997; 97US-0056862.
 PR 22-AUG-1997; 97US-0056864.
 PR 22-AUG-1997; 97US-0056872.
 PR 22-AUG-1997; 97US-0056874.
 PR 22-AUG-1997; 97US-0056875.
 PR 22-AUG-1997; 97US-0056876.
 PR 22-AUG-1997; 97US-0056877.
 PR 22-AUG-1997; 97US-0056878.
 PR 22-AUG-1997; 97US-0056879.
 PR 22-AUG-1997; 97US-0056880.
 PR 22-AUG-1997; 97US-0056881.
 PR 22-AUG-1997; 97US-0056882.
 PR 22-AUG-1997; 97US-0056884.
 PR 22-AUG-1997; 97US-0056886.
 PR 22-AUG-1997; 97US-0056887.
 PR 22-AUG-1997; 97US-0056888.
 PR 22-AUG-1997; 97US-0056889.
 PR 22-AUG-1997; 97US-0056892.
 PR 22-AUG-1997; 97US-0056893.
 PR 22-AUG-1997; 97US-0056894.
 PR 22-AUG-1997; 97US-0056903.
 PR 22-AUG-1997; 97US-0056908.
 PR 22-AUG-1997; 97US-0056909.
 PR 22-AUG-1997; 97US-0056910.
 PR 22-AUG-1997; 97US-0056911.
 PR 05-SEP-1997; 97US-0057650.
 PR 05-SEP-1997; 97US-0057669.
 PR 05-SEP-1997; 97US-0057761.
 PR 12-SEP-1997; 97US-0058785.
 PR (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,
 PI Feng P, Ferrite AM, Fischer CL, Florence KA, Greene JM, Hu JS;
 PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
 XX
 DR WPI: 1998-506364/43.
 DR P-PSDB: AAW74961.
 XX
 PT New isolated human genes and the secreted polypeptide(s) they encode
 PT - useful for diagnosis and treatment of e.g. cancers, neurological
 PT disorders, immune diseases, inflammation or blood disorders
 XX
 PS Claim 1; Page 472; 721pp; English.
 CC
 CC This sequence represents a nucleic acid molecule designated Gene 88 from
 CC the human cDNA clone HAAVY2 (deposited as clone ATCC 97897 and ATCC
 CC 209043) which encodes a secreted human protein. The gene can be used to
 CC generate fusion proteins by linking to the gene to a human
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
 CC the fused protein as compared to the human protein only.

CC The invention relates to 186 novel genes and their fragments (nucleic
 CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
 CC which are useful for preventing, treating or ameliorating medical
 CC conditions e.g. by protein or gene therapy. Also, pathological
 CC conditions can be diagnosed by determining the amount of the new
 CC polypeptides in a sample or by determining the presence of mutations in
 CC the new polynucleotides. Specific uses are described for each of the 186
 CC polynucleotides, based on which tissues they are most highly expressed in
 CC (see AAV59511 for described uses).
 CC
 SQ Sequence 506 BP; 148 A; 103 C; 121 G; 132 T; 2 other;
 alignment_scores:
 Quality: 508.00 Length: 99
 Ratio: 5.131 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000
 alignment_block:
 US-09-801-115-2 x AAV59746 ..
 Align seg 1/1 to: AAV59746 from: 1 to: 506
 1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVal 17
 117 ATGGATATACGTCAGCCGCAAAATATAACATCGCCCTCTGCTTCAAGT 166
 17 IlySGIYHISValLysMetLeuArgLeuAspIleLeuSerLeuValT 34
 167 GAAGGCGCAGTGAGATGCGCTGGATATATATCACTACGCTGTA 216
 34 hTThrValPheMetLeuIleValIserValLeuAlaLeuIleProGluThr 50
 217 CAACAGTATTCATGCTCATCGTATCTGTGTGGCATGTATCCAAAC 266
 51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValC 67
 267 ACAACATTGACAGTGTGGAGGGGTGTTCACCTTGACAGCAGTATG 316
 67 scYsLeuAlaAspGlyAlaLeuIleTyrArgLysLeuPheAsnProS 84
 317 CTGTCTGCCGACGGGCCCTTATTTACCGAGACTTCTGTTCATCCCA 366
 84 eRGlyProTyrGlnLysLysProValHisGluLysLysGluValLeu 99
 367 GCGGCTCTTACCCGAAAGAGCTGTGATGAAAAAGAAAGAGTTTG 413
 seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/NA2000.DAT:AA87730
 seq_documentation_block:
 ID AAA87730 standard; cDNA; 515 BP.
 AC AAA87730;
 XX
 DT 28-NOV-2000 (first entry)
 XX
 DE Human secreted protein encoding cDNA SEQ ID #29.
 XX
 KW Human; secreted protein; forensic procedure; gene therapy;
 KW chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
 KW cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
 KW brain disorder; skeletal muscle disorder; eye disorder; obesity;
 KW mitochondrialcytopathy; diabetes; atherosclerosis; Alzheimer's disease;
 KW neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
 KW septic shock; impotence; ss.
 XX
 OS Homo sapiens.
 OS
 XX
 PN WO200037491-A2.
 XX
 XX 29-JUN-2000.
 PD
 XX
 PF 20-DEC-1999; 99MO-IB02058.

```

XX 22-DEC-1998; 9805-0113686.
PR 25-JUN-1999; 9905-0141032.
XX (GEST ) GENSET.
PI Bougueleret L, Dumas J, Duclert A:
XX WPI: 2000-442637/38.
DR P-PSDB: AAB25768.
XX
XX Polynucleotides and polypeptides encoding proteins with signal
PT peptides, useful in diagnostic, forensic, gene therapy and chromosome
PT mapping procedures -
XX
XX Claim 1, Page 169-170; 306pp; English.
XX
XX This sequence represents human cDNA encoding a secreted protein. The
CC invention relates to sequences AA87725-AA87774 which encode human
CC secreted proteins AAB25763-B25812. The proteins include signal peptides.
CC included in the invention are a host cell containing one of the cDNA
CC sequences, and a purified antibody capable of binding to one of the
CC secreted proteins. Also contained in the invention are methods for
CC storing the sequence data on a computer system, and a method for
CC identifying features of the cDNA sequences using a computer programme.
CC The cDNAs are useful for expressing secreted proteins or fragments to
CC obtain antibodies capable of specifically binding to the secreted
CC proteins. The cDNAs may also be useful in diagnostic, forensic, gene
CC therapy and chromosome mapping procedures and may be used to design
CC expression vectors and secretion vectors. The proteins of the invention
CC may be used to treat diseases including cancer, autoimmune diseases,
CC cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
CC disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye
CC disorders, obesity, mitochondrial cytopathies, diabetes, atherosclerosis,
CC neurodegenerative disorders, graft rejection, Alzheimer's disease,
CC dementia, hyperlipidaemia, septic shock and impotence.
XX
XX Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

alignment_scores:
Quality: 508.00 Length: 99
Ratio: 5.131 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-801-115-2 x AAA87730 ..
Align seg 1/1 to: AAA87730 from: 1 to: 515
1 MetAspAsnValGlnProLysIleLysHisArgProPheGlyPheSerVal 17
|||||
144 ATGATTAACGTCAGCCGCAAAATAAACATGCCCTTGCTTCAGTGT 193
17 llysglyHisVallysmetLeuArgLeuAspIleIleasnSerLeuValT 34
|||||
194 GAAAGGCCACGCTGAAGATGCTGCGGTGATATATCACTCACTGATTA 243
34 hrThValPheMetLeuIleValSerValIleuAlaLeuIleProGluThr 50
|||||
244 CAACAGTATTCATGCTCATCTATCTGTGGCAGCATGATACCAAGAAC 293
51 ThrThrLeuThrValIlglyIlglyValPheAlaLeuValThrAlaValcy 67
|||||
294 ACAACATTTGACAGTTGGTGGAGGGGTTTGGCACTTGTGACAGCATATG 343
67 scYsLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheasnPro 84
|||||
344 CTGCTCTGCGAGCGGGCCCTTATTATACGGAAGCTTCTGTCAATCCA 393
84 ergLysProTyrGlnLysLysProValHisGluLysLysGluValLeu 99
|||||
394 GCGGTCTTACACAGAAAAAGCTGTGCATGAAAAAAGAAATTTTG 440

```

```

seq_name: /SIDSI/gcgcdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAF64012
seq_documentation_block:
ID AAF64012 standard; cDNA; 515 BP.
XX
XX AAF64012;
AC
XX
XX 05-APR-2001 (first entry)
DT
XX
DE cDNA encoding human secreted protein #13.
XX
XX Secreted protein; prevention; treatment; diagnosis; disease;
KW infection; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200100806-A2.
PN
XX
XX 04-JAN-2001.
PD
XX
XX 21-JUN-2000; 2000MO-JB00951.
PF
XX
XX 25-JUN-1999; 9905-0141032.
PR 21-DEC-1999; 9905-0469099.
XX
XX (GEST ) GENSET.
PA
XX
XX Dumas Mline Edwards J, Bougueleret L, Jobert S;
PI
XX
XX WPI: 2001-071487/08.
DR
XX
XX 49 Secreted proteins and the nucleic acids encoding them, useful in
PT gene therapy and for detecting similar sequences in samples -
PT
XX
XX Claim 1, Page 225; 307pp; English.
XX
XX The present invention relates to 49 Secreted proteins and the cDNAs
CC encoding them. The protein and nucleic acids may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate protein expression.
XX
XX Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

alignment_scores:
Quality: 508.00 Length: 99
Ratio: 5.131 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-801-115-2 x AAF64012 ..
Align seg 1/1 to: AAF64012 from: 1 to: 515
1 MetAspAsnValGlnProLysIleLysHisArgProPheGlyPheSerVal 17
|||||
144 ATGATTAACGTCAGCCGCAAAATAAACATGCCCTTGCTTCAGTGT 193
17 llysglyHisVallysmetLeuArgLeuAspIleIleasnSerLeuValT 34
|||||
194 GAAAGGCCACGCTGAAGATGCTGCGGTGATATATCACTCACTGATTA 243
34 hrThValPheMetLeuIleValSerValIleuAlaLeuIleProGluThr 50
|||||
244 CAACAGTATTCATGCTCATCTATCTGTGGCAGCATGATACCAAGAAC 293
51 ThrThrLeuThrValIlglyIlglyValPheAlaLeuValThrAlaValcy 67
|||||
294 ACAACATTTGACAGTTGGTGGAGGGGTTTGGCACTTGTGACAGCATATG 343
67 scYsLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheasnPro 84
|||||

```


344 CTGCTTCCGACGGGGCCCTTATTACGGAGACTTCTGCATCCCA 393
 84 erGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
 394 GCGGTCTTACCAAGAAAAAGCTGTGCATGAAAAAAGAGTTTGG 440
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA38006

seq_documentation_block:
 ID AAA38006 standard; cDNA; 534 BP.

AC AAA38006;

DE 22-AUG-2000 (first entry)

DE UCK-1 nucleotide sequence.

XX UCK-1; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;
 KM radiotherapy; chemotherapy; human; ss.

OS Homo sapiens.

PN CN1244584-A.

PD 16-FEB-2000.

PF 14-MAY-1999; 99CN-0107284.

PR 14-MAY-1999; 99CN-0107284.

PA (UYBE-) UNIT BEIJING MEDICAL.

PI Ma D, Han W, Zhang Y;

DR WPI; 2000-388170/34.

DR P-PSDB; AAY98142.

PT Chemotactic factor useful for treatment and diagnosis of immunocyte

PT disorders - has immunocyte chemotactic stimulating factor

XX Example 4; Fig 1; 31pp; Chinese.

XX This sequence represents an UCK-1 cDNA sequence encoding a chemotaxis

XX factor polypeptide. The UCK-1 protein exhibits immunocyte chemotaxis

XX activity and a haemopoiesis stimulating effect. The invention relates to

XX UCK proteins, their encoding nucleotide sequences and antibodies and

XX antagonists against the proteins. The nucleotide and protein sequences

XX are useful for the preparation of a composition for the diagnosis and

XX treatment of diseases associated with abnormal immunocyte function and

XX low haemopoiesis function caused by radiotherapy and chemotherapy used to

XX treat tumours and other diseases.

XX Sequence 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other;

XX alignment_scores:

XX Quality: 508.00 Length: 99

XX Ratio: 5.131 Gaps: 0

XX Percent Similarity: 100.000 Percent Identity: 100.000

XX alignment_block:

XX US-09-801-115-2 x AAA38006 ..

XX Align seg 1/1 to: AAA38006 from: 1 to: 534

34 hrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
 252 CACACGATATTCATGCTCATCTGTGTGGCAGCTATACGAAAC 301
 51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCy 67
 302 ACAACATTGACAGTGTGGAGGGGTGTGGCACTTGTGACAGCAGTATG 351
 67 scYsLeuAlaAspGlyAlaLeuIleTyrArgLysLeuPheAsnPro 84
 352 CTGTCTTCCGACGGGGCCCTTATTACCGAGAGCTCTGTCAATCCCA 401
 84 erGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
 402 GCGGTCTTACCAAGAAAAAGCTGTGCATGAAAAAAGAGTTTGG 448
 seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH98515

seq_documentation_block:
 ID AAH98515 standard; cDNA; 538 BP.

AC AAH98515;

DE 12-OCT-2001 (first entry)

DE Human EST-derived coding sequence SEQ ID NO: 372.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

XX diagnostics; forensic test; gene mapping; genetic disorder;

XX biodiversity; gene therapy; nutrition; ss.

XX Homo sapiens.

XX WO200154477-A2.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-US02687.

XX 25-JAN-2000; 2000US-0491404.

XX 17-JUL-2000; 2000US-0617746.

XX 03-AUG-2000; 2000US-0631451.

XX 15-SEP-2000; 2000US-0663870.

XX (HYSE-) HYSEQ INC.

XX Tang YF, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

XX Cao Y, Drmanac RA, Zhang J, Werhman T;

XX WPI; 2001-476164/51.

XX P-PSDB; AAM23856.

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

XX antibodies and research use -

XX Claim 1; Page 451; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel

XX proteins from a variety of organisms, including human, dog, cat, horse,

XX cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

XX urchin and tomato. These were derived from expressed sequence tags (ESTs)

XX from the organism of interest. They can be used in diagnostics,

XX forensics, gene mapping, identification of mutations, to assess

XX biodiversity and for nutritional purposes. The present sequence is a cDNA

XX of the invention.

XX Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

XX alignment_scores:

XX Quality: 508.00 Length: 99

XX Ratio: 5.131 Gaps: 0

Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-801-115-2 x AAH98515/rev ..

Align seg 1/1 to reverse of: AAH98515 from: 1 to: 538

```

1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVa 17
  |||||||
366 ATGGATTAACGTCGACGCCGAAATGAAACATCGCCCTTCGCTTCACTGT 317
17 LlysGlyHisValLysMetLeuArgLeuAspIleLeaSerLeuValT 34
  |||||||
316 GAAAGGCCACGTCGAGATGCTGCGCGGATATTATCACTGCTGCTAA 267
34 hrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
  |||||||
266 CAACAGATTATCATGCTCATCTGATCTGTGGCAGCATGACAGCAAAAC 217
51 ThrThrLeuThrValIleGlyGlyValPheAlaLeuValThrAlaValCy 67
  |||||||
216 ACAACATTGACAGTTGGTGGGCGGTGTGCACTTGTGACAGCATATG 167
67 scLysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProS 84
  |||||||
166 CTGCTTGGCCGACGGGCGCTTATTACCGAAGCTTCTGTTCAATCCCA 117
84 erGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
  |||||||
116 GCGGTCCTTACCGAAGAAAGCCTGTCATGAAAAAAGAAAGTTTGG 70

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH98548

seq_documentation_block:

ID AAH98548 standard; cDNA: 538 BP.

AAH98548;

12-OCT-2001 (first entry)

Human EST-derived coding sequence SEQ ID NO: 405.

Human: sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 diagnostics; forensic test; gene mapping; genetic disorder;
 biodiversity; gene therapy; nutrition; ss.

Homo sapiens.

WO200154477-A2.

02-AUG-2001.

25-JAN-2001; 2001WO-US02687.

25-JAN-2000; 2000US-0491404.

17-JUL-2000; 2000US-0617746.

03-AUG-2000; 2000US-0631451.

15-SEP-2000; 2000US-0663870.

(HYSE-) HYSEQ INC.

WPI: 2001-476164/51.

P-PSDB: AAM23889.

Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

Cao Y, Drmanac RA, Zhang J, Werhman T;

Isolated polypeptide for treatment of diseases, diagnostics, raising
 antibodies and research use -

Claim 1; Page 467; 1275pp; English.

CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a cDNA
 CC of the invention.
 CC
 SQ Sequence 538 BP; 141 A; 142 C; 115 G; 140 T; 0 other;

alignment_scores:

quality: 508.00

ratio: 5.131

Percent Similarity: 100.000

Percent Identity: 100.000

alignment_block:

US-09-801-115-2 x AAH98548/rev ..

Align seg 1/1 to reverse of: AAH98548 from: 1 to: 538

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1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVa 17
  |||||||
366 ATGGATTAACGTCGACGCCGAAATGAAACATCGCCCTTCTGCTTCACTGT 317
17 LlysGlyHisValLysMetLeuArgLeuAspIleLeaSerLeuValT 34
  |||||||
316 GAAAGGCCACGTCGAGATGCTGCGCGGATATTATCACTGCTGCTAA 267
34 hrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
  |||||||
266 CAACAGATTATCATGCTCATCTGATCTGTGGCAGCATGACAGCAAAAC 217
51 ThrThrLeuThrValIleGlyGlyValPheAlaLeuValThrAlaValCy 67
  |||||||
216 ACAACATTGACAGTTGGTGGGCGGTGTGCACTTGTGACAGCATATG 167
67 scLysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProS 84
  |||||||
166 CTGCTTGGCCGACGGGCGCTTATTACCGAAGCTTCTGTTCAATCCCA 117
84 erGlyProTyrGlnLysLysProValHisGluLysGluValLeu 99
  |||||||
116 GCGGTCCTTACCGAAGAAAGCCTGTCATGAAAAAAGAAAGTTTGG 70

```

seq_name: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:AAH34835

seq_documentation_block:

ID AAH34835 standard; cDNA: 558 BP.

AAH34835;

03-SEP-2001 (first entry)

Human colon cancer antigen encoding cDNA SEQ ID NO:1917.

Human: colon cancer; colon cancer antigen; diagnosis; detection;
 colorectal carcinoma; ss.

Homo sapiens.

WO200122920-A2.

05-APR-2001.

28-SEP-2000; 2000WO-US26524.

29-SEP-1999; 99US-0157137.

03-NOV-1999; 99US-0163280.

(HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Birse CE, Rosen CA;
 XX WPI: 2001-235357/24.
 DR P-PSDB; AAG75430.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 1; Page 3428; 9803pp; English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAG77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SO Sequence 558 BP; 150 A; 119 C; 145 G; 141 T; 3 other;

alignment_scores:
 Quality: 508.00 Length: 99
 Ratio: 5.131 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
 US-09-801-115-2 x AAH34835 ..

Align seg 1/1 to: AAH34835 from: 1 to: 558

1 MetSpaSnValGlnProLysIleValHisArgProPheCysPheSerVal 17
 |||||||
 147 ATGGATTAACGTCGACGCCGAAATATAACATCGCCCTTGTGCTTCACTGT 196
 |||||||
 17 LlycGlyHisValIysMetLeuArgLeuAspIleIleAsnSerLeuVal 34
 |||||||
 197 GAAAGGCCAGCTGAAGATGCTGGCGGTGGATATATCACTCACTGGTAA 246
 |||||||
 34 hrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
 |||||||
 247 CAAAGATTCATCATCTGATCTATCTGTGGCAGCAGATACCAAGAAC 296
 |||||||
 51 ThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAlaValCy 67
 |||||||
 297 ACAACATTGACACGTTGGTGGAGGGGCTTTGGCACTTGTGACAGCAGATG 346
 |||||||
 347 CTGCTTGGCCGAGCGGGCCCTTATTATTCGGAAGCTTCTGTCAATCCCA 396
 |||||||
 67 sCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnPro 84
 |||||||
 84 ergLysProTyrGlnLysLysProValHisGluLysLysGluValLeu 99
 |||||||
 397 GCGGCTCTTACCAAGAAAGCCTGTCATGAAAAAGAAAGAGTTTGG 443

seq_name: /SDSL/gcgdata/geneseq/geneseqn-embd/NM2001A.DAT:AA544932

seq_documentation_block:
 ID AA544932 standard; CDNA; 655 BP.
 XX
 AC AA544932;

XX
 DT 18-DEC-2001 (first entry)
 XX
 DE CDNA encoding novel human secretory protein, Seq ID No 13.
 XX
 KM Human; secreted protein; arthritis; Crohn's disease; sepsis; shock;
 KM Ischaemia-reperfusion injury; haematopoiesis; cancer; neuropathy;
 KM transgenic animal; Alzheimer's disease; Parkinson's disease; burn;
 KM amyotrophic lateral sclerosis; platelet disorder; thrombocytopenia;
 KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease;
 KM gut protection; lung; liver fibrosis; immune deficiency; infection;
 KM severe combined immunodeficiency; SCID; autoimmune disorder; allergy;
 KM multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;
 KM fertility; analgesic; pain; antigen; ss.
 OS Homo sapiens.
 XX
 PM WO20016689-A2.
 XX
 PD 13-SEP-2001.
 XX
 PF 05-MAR-2001; 2001WO-US04942.
 XX
 PR 07-MAR-2000; 2000US-0519705.
 PR 19-MAY-2000; 2000US-0574454.
 PR 17-JUN-2000; 2000US-0596193.
 PR 14-JUL-2000; 2000US-0616847.
 PR 19-SEP-2000; 2000US-0665363.
 PR 20-OCT-2000; 2000US-0693267.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Xu C, Wehrman T, Ren F, Ma Y, Zhou P;
 PI Zhao QA, Yang Y, Drmanac RT, Zhang J, Chen R, Xue AJ, Wang J;
 XX
 DR WPI: 2001-589934/66.
 DR P-PSDB; AAU28032.
 XX
 PT Novel polypeptides and nucleic acids obtained from CDNA libraries
 prepared from various human tissues, for diagnosis and treatment of
 PT cancer, neurological, inflammatory, and autoimmune disorders -
 XX
 PS Claim 1; SEQ ID No 13; 107pp; English.

The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating disease, inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the in vivo activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides

CC analgesic effects or other pain reducing effects, immunoglobulin like
 CC activity and can act as an antigen in a vaccine composition to raise an
 CC immune response. AAS44920-AAS45295 represent novel human secreted protein
 CC coding sequences of the invention.

XX Sequence 655 BP; 178 A; 129 C; 181 G; 167 T; 0 other;

alignment_scores:

Quality: 508.00 Length: 99
 Ratio: 5.131 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:

US-09-801-115-2 x AAS44932 ..

Align seg 1/1 to: AAS44932 from: 1 to: 655

```

1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVa 17
|||||
134 ATGGATTAACGTGCGAGCGAAATATAACATCGCCCTTCTGCTCAGTGT 183
17 IlySGlyHisValLysMetLeuArgLeuAspIleIleAsnSerLeuValT 34
|||||
184 GAAAGGCCACGTGAAGATGCTGCGCTGATATATCACTCACTCGTAA 233
34 hrtHrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
|||||
234 CAACAGTATTATGCTCATCTATCTGTGTGGACGTGATACCGAANCC 283
51 ThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAlaValCy 67
|||||
284 ACAACATTGACAGTTGGTGGAGGGGTGTTCCTGCTGGACAGCATATG 333
67 scyLeuAlaLaspIlyAlaLeuIleTyrArgLysLeuLeuPheAsnProS 84
|||||
334 CTGCTTGGCCGACGGGGCCCTTATTACCGGAACCTCTGTTCAATCCA 383
84 ergLProTyrGlnLysLysProValHisGluLysLysGluValLeu 99
|||||
384 GCGGCTCTTACCAGAAAAGCCTGTGCATGAAAAAGAAAGTTTGG 430

```

seq_name: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AAA15919

seq_documentation_block:

ID AAA15919 standard; cDNA; 297 BP.

XX AAA15919;

DT 12-JUN-2000 (first entry)

XX Human protein clone HP10357 coding sequence.

XX Human protein; hydrophobic domain; nutritional source; haematopoiesis;
 KW cytokine production; cell proliferation; cell differentiation;
 KW immune deficiency; infectious disease; autoimmune disorder; asthma;
 KW multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
 KW allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
 KW nervous system disorder; Alzheimer's disease; Parkinson's disease;
 KW Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
 KW systemic cytokine damage; tissue differentiation; contraceptive; stroke;
 KW coagulation disorder; myocardial infarction; inflammatory condition;
 KW septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
 KW nephritis; therapy; ss.

XX Homo sapiens.

XX W0200005367-A2.

XX 03-FEB-2000.

XX 22-JUL-1999; 99WO-JP03929.

PR 24-JUL-1998; 98JP-0208820.
 PR 07-AUG-1998; 98JP-0224105.
 PR 25-AUG-1998; 98JP-0238116.
 PR 09-SEP-1998; 98JP-0254736.
 PR 29-SEP-1998; 98JP-0275505.

PA (SAGA) SAGAMI CHEM RES CENT.
 PA (PROT-) PROTEGENE INC.

XX Kato S, Kimura T;

XX WPI: 2000-182694/16.

XX P-PsDB: AAY94861.

PT Novel human proteins having hydrophobic domains useful for treating
 PT osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
 PT multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
 PS Claim 3; Page 217-218; 351pp; English.

CC This sequence encodes a human protein of the invention, which has
 CC hydrophobic domains. The DNA sequences can be used as a probe or as a
 CC genetic marker. The protein can also be used as a marker, and to identify
 CC potential genetic disorders. The DNA and protein can also be used as
 CC nutritional sources or supplements. The protein exhibits cytokine, cell
 CC proliferation, cell differentiation activities and induces production of
 CC other cytokines in certain cell populations. The protein also exhibits
 CC immune stimulating or immune suppressing activity. It can be used in the
 CC treatment of various immune deficiencies and disorders, and to treat
 CC infectious diseases caused by viral, bacterial, fungal or other
 CC infections. The protein is also used for treating autoimmune disorders
 CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
 CC arthritis. It is also useful in the treatment of allergic reactions and
 CC conditions such as asthma, and in immune suppression after organ
 CC transplantation. The protein is useful in regulation of haematopoiesis
 CC and consequently in the treatment of myeloid or lymphoid cell
 CC deficiencies. It is also used in compositions for tissue growth or
 CC regeneration. The protein is also used in the treatment of osteoporosis
 CC or osteoarthritis and in the treatment of periodontal disease and other
 CC tooth repair processes. The protein is used in the treatment of nervous
 CC system disorders such as Alzheimer's disease, Parkinson's disease, and
 CC Huntington's disease. They are useful for protection or regeneration and
 CC treatment of lung or liver fibrosis, reperfusion injury in various
 CC tissues, and conditions resulting from systemic cytokine damage. They are
 CC also used for promoting or inhibiting tissue differentiation. They are
 CC also used as contraceptives since they exhibit activin or inhibin related
 CC activities and as a fertility inducing therapeutic. They are used for
 CC treating various coagulation disorders and in treatment and prevention of
 CC conditions resulting from coagulation activities e.g. myocardial
 CC infarction or stroke. They also acts as receptors, receptor ligands or
 CC inhibitors or agonists of receptor/ligand interactions. They are used to
 CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
 CC reperfusion injury, arthritis, and nephritis. They can be used to
 CC prevent tumours.

XX Sequence 297 BP; 81 A; 68 C; 72 G; 76 T; 0 other;

alignment_scores:

Quality: 504.00 Length: 99
 Ratio: 5.091 Gaps: 0
 Percent Similarity: 100.000 Percent Identity: 98.990

alignment_block:

US-09-801-115-2 x AAA15919 ..

Align seg 1/1 to: AAA15919 from: 1 to: 297

```

1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVa 17
|||||
1 ATGGATTAACGTGCGAGCGAAATATAACATCGCCCTTCTGCTCAGTGT 50
17 IlySGlyHisValLysMetLeuArgLeuAspIleIleAsnSerLeuValT 34

```

```

|||||
51 GAAAGGCCACGTGAAGATGCTGCGCTGGATATATCAACACTCGGTAA 100
34 hrrThrValPheMetLeuIleValSerValIleAlaLeuIleProGluThr 50
101 CAACGATATCATGCTCATCTGATCTGTGTTGGACATGATCCGAAAC 150
51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
151 ACAACATTTGACAGTTGGTGGAGGGGTGTTTGCCTTGGACAGCAGTATG 200
67 scYsLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProS 84
201 CTGCTTTCGCCAGCGGGCCCTTATTACCGGAACCTTCTGTCAATCCCA 250
84 erGlyProTyrGlnLysLysProValHisGluLysGluValIleu 99
251 GCGGCTCTTACCAGCAAAAGCCTGTGCTGTAAGAAAAAGAAAGTTTGG 297

seq_name: /SIDSl/gcgdata/geneseq/geneseqn-emb1/NA15929
seq_documentation_block:
ID AAA15929 standard; cDNA; 467 BP.
XX
XX AAA15929;
XX
XX 12-JUN-2000 (first entry)
XX
XX Human protein clone HP10357 full length coding sequence.
XX
XX Human protein; hydrophobic domain; nutritional source; haematopoiesis;
XX cytokine production; cell proliferation; cell differentiation;
XX immune deficiency; infectious disease; autoimmune disorder; asthma;
XX multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis;
XX allergic reaction; osteoporosis; osteoarthritis; periodontal disease;
XX nervous system disorder; Alzheimer's disease; Parkinson's disease;
XX Huntington's disease; liver fibrosis; lung fibrosis; reperfusion injury;
XX systemic cytokine damage; tissue differentiation; contraceptive; stroke;
XX coagulation disorder; myocardial infarction; inflammatory condition;
XX septic shock; sepsis; ischaemia; reperfusion injury; arthritis; tumour;
XX nephritis; therapy; ss.
XX
XX Homo sapiens.
XX
XX WO200005367-A2.
XX
XX 03-FEB-2000.
XX
XX 22-JUL-1999: 99WO-JP03929.
XX
XX 24-JUL-1998: 98JP-0208820.
XX 07-AUG-1998: 98JP-0224105.
XX 25-AUG-1998: 98JP-0238116.
XX 09-SEP-1998: 98JP-0254736.
XX 29-SEP-1998: 98JP-0275505.
XX
XX (SAGA ) SAGAMI CHEM RES CENT.
XX (PROT-) PROTEGENE INC.
XX
XX Kato S, Kimura T:
XX
XX WPI, 2000-182694/16.
XX P-PSDB; AAY94861.
XX
XX Novel human proteins having hydrophobic domains useful for treating
XX osteoporosis, Alzheimer's disease, Parkinson's disease, asthma,
XX multiple sclerosis, rheumatoid arthritis, cancer, anaemia, and stroke -
XX
XX Claim 4: Page 228; 351pp; English.
XX
XX This sequence encodes a human protein of the invention, which has
XX hydrophobic domains. The DNA sequences can be used as a probe or as a
XX genetic marker. The protein can also be used as a marker, and to identify

```

```

CC potential genetic disorders. The DNA and protein can also be used as
CC nutritional sources or supplements. The protein exhibits cytokine, cell
CC proliferation, cell differentiation activities and induces production of
CC other cytokines in certain cell populations. The protein also exhibits
CC immune stimulating or immune suppressing activity. It can be used in the
CC treatment of various immune deficiencies and disorders, and to treat
CC infectious diseases caused by viral, bacterial, fungal or other
CC infections. The protein is also used for treating autoimmune disorders
CC such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid
CC arthritis. It is also useful in the treatment of allergic reactions and
CC conditions such as asthma, and in immune suppression after organ
CC transplantation. The protein is useful in regulation of haematopoiesis
CC and consequently in the treatment of myeloid or lymphoid cell
CC deficiencies. It is also used in compositions for tissue growth or
CC regeneration. The protein is also used in the treatment of osteoporosis
CC or osteoarthritis and in the treatment of periodontal disease and other
CC tooth repair processes. The protein is used in the treatment of nervous
CC system disorders such as Alzheimer's disease, Parkinson's disease, and
CC Huntington's disease. They are useful for protection or regeneration and
CC treatment of lung or liver fibrosis, reperfusion injury in various
CC tissues, and conditions resulting from systemic cytokine damage. They are
CC also used for promoting or inhibiting tissue differentiation. They are
CC also used as contraceptives since they exhibit activin or inhibin related
CC activities and as a fertility inducing therapeutic. They are used for
CC treating various coagulation disorders and in treatment and prevention of
CC conditions resulting from coagulation activities e.g. myocardial
CC infarction or stroke. They also acts as receptors, receptor ligands or
CC inhibitors or agonists of receptor/ligand interactions. They are used to
CC treat inflammatory conditions such as septic shock, sepsis, ischaemia
CC reperfusion injury, arthritis, and nephritis. They can be used to
CC prevent tumours.
XX
XX
XX Sequence 467 BP; 118 A; 101 C; 121 G; 127 T; 0 other:

```

```

alignment_scores:
Quality: 504.00 Length: 99
Ratio: 5.091 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.990

```

alignment_block:

us-09-801-115-2 x AAA15929

Align seg 1/1 to: AAA15929 from: 1 to: 467

```

1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVal 17
114 ATGATATACGTGACGCGGAATAAATCAATCGCCCTTCTGCTCAGTCT 163
17 LysGlyHisValLysMetLeuArgLeuAspIleIleAsnSerLeuValT 34
164 GAAAGGCCACGTGAAGATGCTGCGCTGGATATATCAACTCAGCTGTA 213
34 hrrThrValPheMetLeuIleValSerValIleAlaLeuIleProGluThr 50
214 CAACATATTCATGCTCATCTGATCTGTGTTGGACATGATACCAAAAC 263
51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCys 67
264 ACAACATTTGACAGTTGGTGGAGGGGTGTTTGCCTTGGACAGCAGTATG 313
67 scYsLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProS 84
314 CTGCTTTCGCCAGCGGGCCCTTATTACCGGAACCTTCTGTCAATCCCA 363
84 erGlyProTyrGlnLysLysProValHisGluLysGluValIleu 99
364 GCGGCTCTTACCAGCAAAAGCCTGTGCTGTAAGAAAAAGAAAGTTTGG 410

```

seq_name: /SIDSl/gcgdata/geneseq/geneseqn-emb1/NA1599, DAT: AAX97826

seq_documentation_block:

ID AAX97826 standard; cDNA: 500 BP.

```

XX  AAX97826;
AC
XX  23-SEP-1999 (first entry)
XX
XX  Human secreted protein encoding CDNA #14.
DE
XX  Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;
KW  diagnostic; gene therapy; chromosome mapping; secretion vector; ss.
XX
XX  Homo sapiens.
OS
XX  W09925825-A2.
PN
XX  27-MAY-1999.
PD
XX
XX  13-NOV-1998; 98MO-IB01862.
PF
XX
XX  04-SEP-1998; 98US-0099273.
PR  13-NOV-1997; 97US-0066677.
PR  17-DEC-1997; 97US-0069957.
PR  09-FEB-1998; 98US-0074121.
PR  13-APR-1998; 98US-0081563.
PR  10-AUG-1998; 98US-0096116.
XX
XX  (GEST ) GENSET.
XX
XX  Bougueleret L, Duclert A, Dumas Milne Edwards J;
PI  MPI; 1999-347472/29.
XX
XX  P-PSDB; AAY36142.
DR
XX
XX  Extended cDNAs encoding secreted proteins
PT
XX
XX  Example 28; Page 173-174; 307pp; English.
PS
XX
XX  AAX97813-X97906 represent extended CDNA's which encode novel human
CC  secreted proteins (see AAY36129-Y36222) and which have cytosolic,
CC  thrombotic and osteopathic activity. The extended cDNAs can be used to
CC  express secreted proteins or parts of them or to obtain antibodies
CC  capable of binding to the secreted proteins. They may also be used in
CC  diagnostic, forensic, gene therapy and chromosome mapping procedures.
CC  Uses also include design of expression vectors and secretion vectors.
XX
XX
XX  Sequence 500 BP; 135 A; 102 C; 125 G; 129 T; 9 other;
SQ

```

alignment_scores:

Quality:	489.00	Length:	100
Ratio:	4.990	Gaps:	1
Percent Similarity:	98.000	Percent Identity:	98.000

alignment_block:

US-09-801-115-2 x AAX97826 ..

Align seg 1/1 to: AAX97826 from: 1 to: 500

```

1  MetAspAsnValGlnProLysIleLysHisArgProPhCySPheserVa 17
   |||||||
132 ATGGTAAACGTGCGAGCCGAAATAAACATCGCCCTTCTGCTCAGTGT 181
   |||||||
17  LlysGlyHisVal.LysMetLeuArgLeuAspIleIleAsnSerLeuVal 33
   |||||||
182 GAAAGGCCACGTGAGTAGTGTGCGGCGGATATATCACTCACTGCTGTA 231
   |||||||
34  ThrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluTh 50
   |||||||
232 ACAACAGATATCATGCTCATGCTATCTGTGTGCACTGATACAGAAAC 281
   |||||||
50  rThrThrLeuThrValGlyGlyGlyValPheAlaLeuValThrAlaValC 67
   |||||||
282 CACAACATGTGACAGTGTGTGAGGGGTGTGTGCACTGTGTGACAGCA 331
   |||||||

```

```

67  yScysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuPheAsnPro 83
   |||||||
332 GCTGTCTTGCCGAGCGGGCCCTTATTTACCGAAGCTTCTGTCAATCCC 381
   |||||||
84  SerGlyProGlyGlnLysLysProValHisGlnLysLysGluValLeu 99
   |||||||
382 AGCGGTCTTACCGAGAAAGCCGTGTCATGAAAAAAGAAAGATTTTGG 429
   |||||||
seq_name: /SIDSI/gc9data/geneseq/geneseqn-emb1/NA2000.DAT:AAA38007

```

seq_documentation_block:

ID AAA38007 standard; CDNA; 459 BP.

XX AAA38007;

AC

XX 22-AUG-2000 (first entry)

DT

XX

DE UCK-2 nucleotide sequence.

XX

XX UCK-2; chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;

KW radiotherapy; chemotherapy; human; ss.

KW

XX

OS Homo sapiens.

XX

PN CN1244584-A.

XX

XX 16-FEB-2000.

PD

XX

PF 14-MAY-1999; 99CN-0107284.

XX

PR 14-MAY-1999; 99CN-0107284.

XX

PA (UYBE-) UNIV BEIJING MEDICAL.

XX

PI Ma D, Han W, Zhang Y;

XX

DR MPI: 2000-388170/34.

XX

XX P-PSDB; AAY98143.

DR

XX

PT Chemotactic factor useful for treatment and diagnosis of immunocyte

PT disorders - has immunocyte chemotactic stimulating factor

XX

PS Example 4; Fig 2; 31pp; Chinese.

XX

XX This sequence represents an UCK-2 cDNA sequence encoding a chemotaxis

CC factor polypeptide. The UCK-2 protein exhibits immunocyte chemotaxis

CC activity and a haemopoiesis stimulating effect. The invention relates to

CC UCK proteins, their encoding nucleotide sequences and antibodies and

CC antagonists against the proteins. The nucleotide and protein sequences

CC are useful for the preparation of a composition for the diagnosis and

CC treatment of diseases associated with abnormal immunocyte function and

CC low haemopoiesis function caused by radiotherapy and chemotherapy used to

CC treat tumours and other diseases.

XX

SQ Sequence 459 BP; 123 A; 99 C; 96 G; 141 T; 0 other;

alignment_scores:

Quality:	471.50	Length:	152
Ratio:	4.763	Gaps:	1
Percent Similarity:	65.132	Percent Identity:	65.132

alignment_block:

US-09-801-115-2 x AAA38007 ..

Align seg 1/1 to: AAA38007 from: 1 to: 459

```

1  MetAspAsnValGlnProLysIleLysHisArgProPhCySPheserVa 17
   |||||||
1  ATGGATTAACGTGCGAGCCGAAATAAACATCGCCCTTCTGCTCAGTGT 50
   |||||||
17  LlysGlyHisValLysMetLeuArg..... 25
   |||||||

```

51 GAAAGCCAGCTGAAGATGCTGGGGTGGCACTAACTGTCATCTATGA 100
 25 25
 101 CCTTTTATCATCGACAAAGCCCTGACCATATATTTGTAATCACTGA 150
 25 25
 151 TTGATGATCACCCCTATCTATTTTCACTACTTTATATGACTACAGACT 200
 26 LeuAspIleIleAsn 31
 201 TGATGATTAATGAAGTGTATTTGGCCCTTGCTGATATATATCAACT 250
 31 erLeuValThrThrValPheMetLeuIleValSerValIleuAlaLeuIle 47
 251 CACGTGGTACACACAGATTCATGCTCATGCTATCTGTTGGCAGCTGATA 300
 48 ProGluThrThrThrLeuThrValIleGlyIleValPheAlaLeuValTh 64
 301 CCAGAAACCAACACATTGACAGTTGGTGGAGGGGTGTTGCACCTGTGAC 350
 64 rAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuP 81
 351 AGCAGTATGCTGCTCTCCGACGGGCCCTTATTTACCGAAGCTCTGT 400
 81 heAsnProSerGlyProTyrGlnLysLysProValHisGluLysGlu 97
 401 TCATCCCAAGCGGTCTTACACGAAAGCCCTGTGCATGAAAGAAAAAGAA 450
 98 ValLeu 99
 451 GTTTTG 456

seq_name: /SDSL/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:AA256747

seq_documentation_block:

ID AA256747 standard; cDNA; 637 BP.

XX AA256747;

DT 23-MAR-2000 (first entry)

DE Human transmembrane protein HTPN-50 encoding cDNA.

XX Human: transmembrane protein; HTPN; diagnosis; immunospecific;

KW antiproliferative; neuroprotective; immune disorder;

KW reproductive disorder; smooth muscle disorder; neurological disorder;

KW gastrointestinal disorder; developmental disorder;

KW cell proliferative disorder; ss.

XX Homo sapiens.

XX OS

XX PN

XX MO961471-A2.

XX 02-DEC-1999.

XX PD

XX 28-MAY-1999; 99WO-US11904.

XX PF

XX 29-MAY-1998; 98US-0087260.

XX PR

XX 02-JUL-1998; 98US-0091674.

XX PR

XX 24-OCT-1998; 98US-0102954.

XX PR

XX 24-NOV-1998; 98US-0109869.

XX PA

XX (INCY-) INCYTE PHARM INC.

XX PI

XX Tang YT, Lal P, Hillman JL, Yue H, Guegler KJ, Corley NC;

XX PI Bandman O, Patterson C, Gorgone GA, Kaser MR, Baughn MR;

XX PI Au-Young J;

XX DR WPI: 2000-072605/06.

XX DR P-PSDB; AAY57926.

XX XX

PT Proteins, polynucleotides, vectors, host cells and antibodies used to
 PT diagnose, treat or prevent immune, reproductive, smooth muscle,
 PT neurological, gastrointestinal, developmental and cell proliferative
 PT disorders -

XX Claim 9; Page 210; 229pp; English.

XX AA25698 to AA256776 encode AAY57877 to AAY57955 which represent human
 CC transmembrane proteins designated HTPN-1 to HTPN-79, respectively.
 CC The transmembrane protein have immunospecific, antiproliferative and
 CC neuroprotective activities. The human transmembrane proteins,
 CC polynucleotides encoding them and other compositions and methods from
 CC the present invention, can be used for the diagnosis, treatment or
 CC prevention of immune, reproductive, smooth muscle, neurological,
 CC gastrointestinal, developmental and cell proliferative disorders. The
 CC HTPN's can be used to treat or prevent disorders associated with a
 CC decreased expression or activity of HTPN.

SQ Sequence 637 BP; 169 A; 134 C; 143 G; 191 T; 0 other;

alignment_scores:

Quality: 471.50 Length: 152
 Ratio: 4.763 Gaps: 1
 Percent Similarity: 65.132 Percent Identity: 65.132

alignment_block:

US-09-801-115-2 x AA256747 ..

Align seg 1/1 to: AA256747 from: 1 to: 637

1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVal 17
 111 ATGGATATACGTGACGCGGAAATTAACATCCGCCCTTCTGCTTCAAGTGT 160
 17 LysGlyHisValLysMetLeuArg..... 25
 161 GAAAGCCACGATGAGATGCTGGCGCTGACACTAGCTGACATCTATGA 210
 25 25
 211 CCTTTTATCATCGCACAAAGCCCTGAAACCATATATGTTATCACTGGA 260
 25 25
 261 TTGAGATCACCGTATCTTATTTTCACTATTATATGACTACAGACT 310
 26 LeuAspIleIleAsn 31
 311 TGATGATTAATGAAGTGTATTTTGGCCCTTGCTGATATATCAACT 360
 31 erLeuValThrThrValPheMetLeuIleValSerValIleuAlaLeuIle 47
 361 CACTGTACACACAGATTCATGCTCATGCTATCTGTGGCAGCTGATA 410
 48 ProGluThrThrThrLeuThrValIleGlyIleValPheAlaLeuValTh 64
 411 CCAGAAACCAACATTTGACAGTTGGTGGAGGGGTGTTGGCACTGTGAC 460
 64 rAlaValCysCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuP 81
 461 AGCAGTATGCTGCTTCCGACGGGCCCTTATTTACCGGAAGCTTCTGT 510
 81 heAsnProSerGlyProTyrGlnLysLysProValHisGluLysGlu 97
 511 TCATCCCAAGCGGTCTTACACGAAAGCCCTGTGCATGAAAGAAAAAGAA 560
 98 ValLeu 99
 561 GTTTTG 566

394 GCGGCTTACCAGAAAAGCCTGTGCATGAAAGAGTTTGG 440

seq_name: gb_pr:AF096895

seq_documentation_block:

LOCUS AF096895 530 bp mRNA linear PRI 18-JUL-2001
DEFINITION Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.
ACCESSION AF096895
VERSION AF096895.2 GI:9989691
KEYWORDS FLI-CDNA.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 530)
AUTHORS Han, W., Lou, Y., Tang, J., Zhang, Y., Chen, Y., Li, Y., Gu, W., Huang, J.,
Gul, D., Tang, Y., Li, F., Song, Q., Di, C., Wang, L., Shi, Q., Sun, R.,
Xia, D., Rui, M., Tang, J., and Ma, D.
Molecular cloning and characterization of chemokine-like factor 1
(CKLF1), a novel human cytokine with unique structure and potential
chemotactic activity
Biochem J. 357 (Pt 1), 127-135 (2001)

JOURNAL MEDLINE
PUBMED 21308461
11415443

REFERENCE 2 (bases 1 to 530)
AUTHORS Han, W. L., Li, Y., Zhang, Y. M., Di, C. H., Song, Q. S. and Ma, D. L.
TITLE Direct Submission
JOURNAL Submitted (03-OCT-1998) Immunology, Beijing Medical University, 38
Xue Yuan Rd., Beijing 100083, China
3 (bases 1 to 530)

REFERENCE 3 (bases 1 to 530)
AUTHORS Han, W. L.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
Sequence update by submitter
On Sep 7, 2000 this sequence version replaced gi:6288733.

REMARK COMMENT
FEATURES
source
1. 530
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/note="exposed to phytohemagglutinin (PHA)"

gene
1. 530
/gene="CKLF1"
/note="DCK-1"
148. 447
/gene="CKLF1"
/note="increased expression in PHA stimulated cells;
expression inhibited by IL-10"

CDS
/codon_start=1
/product="chemokine-like factor 1"
/protein_id="AA06722.1"
/db_xref="GI:6288732"
/translation="MDNVOPKIKHRPFCVSKGHVKMLRLDINSITVTEMLIVSYLV
ALIPETITLVGGVAVLTAVCCADGALIRKLLENPSGPKPKVHEKEVL"

BASE COUNT 156 a 108 c 137 g 129 t
ORIGIN

alignment_scores:
Quality: 508.00 Length: 99
Ratio: 5.131 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment_block:
US-09-801-115-2 x AF096895 ..

Align seg 1/1 to: AF096895 from: 1 to: 530

1 MetaspasnaValGlnProLysIleLysHisArgProPheCysPheSerVa 17
|||||
148 ATGGATTAACGTCGACGCCGAAATTAACATCGCCCTTCTGCTTCACTGT 197

17 LTVSGLYHISVALLYMERTLEUARGLEUASPILLEILEASNSERTLEUValT 34
|||||
198 GAAAGGCCACGTGATGCTGCGCTGATATTATCACTACCTGTGTA 247

34 hThrValPheMetLeuIleValSerValLeuAlaLeuLeuProGluThr 50
|||||
248 CAACAGATTCATGCTCATGATGATGCTGTGGTGGCACTGATACAGAAAC 297

51 ThThLeuThrValGlyGlyValPheAlaLeuValThAlaValcy 67
|||||
298 ACAACATTGACAGTGTGAGGGGTGTTCGACTGTGACAGCAGTATG 347

67 scYsLeuAlaAspGlyAlaLeuLeuLeuLeuLeuLeuLeuLeuLeu 84
|||||
348 CTCTCTTCCGACGAGGCGCCCTTTATCCGGAAGCTTCTGTTCAATCC 397

84 exGlyProTyGlnLysLysProValHisGluLysGluValLeu 99
|||||
398 GCGGCTTACCAGAAAAGCCTGTGCATGAAAGAGTTTGG 444

seq_name: gb_pr:AF057306
seq_documentation_block:
LOCUS AF057306 655 bp mRNA linear PRI 31-DEC-1999
DEFINITION Homo sapiens transmembrane proteolipid (C32) mRNA, complete cds.
ACCESSION AF057306
VERSION AF057306.1 GI:6648618
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 655)
AUTHORS Zhang, J. S., Nelson, M., Wang, L. and Smith D. I.
TITLE Direct Submission
JOURNAL Submitted (03-APR-1998) Pathology and Lab. Medicine, Mayo Clinic
and Foundation, Rochester, MN 55905, USA
Location/Qualifiers

source
1. 655
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="AsPC-1"
/tissue_type="pancreas"
/note="adenocarcinoma"

gene
1. 655
/gene="C32"
132. 590
/gene="C32"
/note="down regulated upon cell differentiation induced by
sodium butyrate"

CDS
/codon_start=1
/product="transmembrane proteolipid"
/protein_id="AA02125.1"
/db_xref="GI:6648619"
/translation="MDNVOPKIKHRPFCVSKGHVKMLRLALTVTSMTEFFITAAQDEP
YIVTGEVTVILFFILLVLRDLRKLKMLFNPDLINSITVTEMLIVSYVALTPE
TTTLTVGGVAVLTAVCCADGALIRKLLENPSGPKPKVHEKEVL"

BASE COUNT 171 a 137 c 153 g 194 t
ORIGIN

alignment_scores:
Quality: 471.50 Length: 152
Ratio: 4.763 Gaps: 1
Percent Similarity: 65.132 Percent Identity: 65.132

alignment_block:
US-09-801-115-2 x AF057306 ..

Align seg 1/1 to: AF057306 from: 1 to: 655

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|||||
148 ATGGATTAACGTCGACGCCGAAATTAACATCGCCCTTCTGCTTCACTGT 197

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|||||
132 ATGATTAACGTACAGCCGAAATAAACAATGCGCCCTTCTGCTTACGTCT 181
17 11ysg1yhi5val1ysmetleuarg..... 25
182 GAAAGGCCACGTGAGATGCTGCGCTGGCACTACTGTCATCTATGATG 231
25 ..... 25
232 CCTTTTATATCATGCGACAGCCCTGTAACATATATTGTTATCACTGGA 281
25 ..... 25
282 TTGAAGTCACCGTTATCTTATTTTCACTTTATATGACTACAGCT 331
26 ..... 31
332 TGATGATTAATGAGTGTTATTTGGCTTGTCTGATATTATCACT 381
31 erleuval1thrthrval1phemetleu1levalserval1leuval1le 47
|||||
382 CACTGTGTAACAACAGTATTCTCATCTCATCTGATCTGTGTGGCACTGATA 431
48 Proglut1thrthrleuthrval1gly1gly1val1phealaleuval1th 64
|||||
432 CCAGAAACCAACAACATGACAGTTGTGGAGGGGTTTGCACCTTGTGAC 481
64 r1alaval1cys1leu1alasp1ylalaleu1le1y1arg1ysleu1eup 81
|||||
482 AGCACTATGCTGTCTTGGCGAGGGGCCCTTATTTACCGAAGCTTCTGT 531
81 heasnProserGlyProTyrglnLysProvalHisglulys1ysglu 97
|||||
532 TCAATCCCAAGCGGTCCTTACCAAGAAAAGCCTGTGCATGAAAAAAGAA 581
98 val1eu 99
|||||
582 GTTTTG 587

seq_name: gb_pat:AX061665

seq_documentation_block:
LOCUS AX061665 669 bp DNA linear PAT 24-JAN-2001
DEFINITION Sequence 70 from Patent WO0100806.
ACCESSION AX061665
VERSION AX061665.1 GI:12406789
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 669)
AUTHORS dumas mlne Edwards,J.B., Bougueleret,L. and Jobert,L.S.
TITLE Complementary dna's encoding proteins with signal peptides
JOURNAL Patent: WO 0100806-A 70 04-JAN-2001;
GENSET (FR)
FEATURES
source location/Qualifiers
1..669
/organism="Homo sapiens"
/db_xref="taxon:9606"
140..598
/feature="unnamed protein product"
/feature="start=1"
/feature="id="CAC25025.1"
/feature="GI:12406790"
/feature="translation="MDNVPKIKHRPFSYGVHVKMLRLALVTSMFTFIQAPEP
YVINGFEVTLIFLLVLRDLRMKMLFPLDINSLVTVFMILVSVLALIP
TTTTLVGGGVFALVAVCCCLADGALIRKLFPNGSPQKRVHKKVEL"
140..442
/feature="Von Heijne matrix score 4.10 seq VMLIVSVLALIP/ET"
polya_signal 630..635
polya_site 655..669
BASE COUNT 178 a 139 c 158 g 194 t

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ORIGIN
alignment_scores:
Quality: 471.50 Length: 152
Ratio: 4.763 Gaps: 1
Percent Similarity: 65.132 Percent Identity: 65.132

alignment_block:
us-09-801-115-2 x AX061665 ..

Align seg 1/1 to: AX061665 from: 1 to: 669

1 Metaspasnval1glnProlys1leLysHisargProPheCysPheSer17
|||||
140 ATGATTAACGTGACGCGGAAATAAACAATGCGCCCTTGTCTGCTTACGT 189
17 11ysg1yhi5val1ysmetleuarg..... 25
|||||
190 GAAAGGCCACGTGAGATGCTGCGCTGGCACTACTGTCATCTATGATA 239
25 ..... 25
240 CCTTTTATATCATGCGACAGCCCTGTAACATATATTGTTATCACTGGA 289
25 ..... 25
290 TTGAAGTCACCGTTATCTTATTTTCACTTTTATATGACTACAGCT 339
26 ..... 31
340 TGATGATTAATGAGTGTTATTTGGCTTGTCTGATATTATCACT 389
31 erleuval1thrthrval1phemetleu1levalserval1leuval1le 47
|||||
390 CACTGTGTAACAACAGTATTCTCATCTCATCTGATCTGTGTGGCACTGATA 439
48 Proglut1thrthrleuthrval1gly1gly1val1phealaleuval1th 64
|||||
440 CCAGAAACCAACAACATGACAGTTGTGGAGGGGCTTGTGCACCTTGTGAC 489
64 r1alaval1cys1leu1alasp1ylalaleu1le1y1arg1ysleu1eup 81
|||||
490 AGCACTATGCTGTCTTGGCGAGGGGCCCTTATTTACCGAAGCTTCTGT 539
81 heasnProserGlyProTyrglnLysProvalHisglulys1ysglu 97
|||||
540 TCAATCCCAAGCGGTCCTTACCAAGAAAAGCCTGTGCATGAAAAAAGAA 589
98 val1eu 99
|||||
590 GTTTTG 595

seq_name: gb_pr:BC004380

seq_documentation_block:
LOCUS BC004380 688 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, clone MGC:10658 IMAGE:3639550, mRNA, complete cds.
ACCESSION BC004380
VERSION BC004380.1 GI:13325133
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 688)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (12-MAR-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov

```

COMMENT

Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@cgsc.bc.ca
Steven Jones, Jennifer Asano, Ian Boedert, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Keta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carlie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LINL at: <http://image.linl.gov>
Series: IRAL Plate: 13 Row: f Column: 14
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 9989692.

FEATURES

source

1..688
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:10658 IMAGE:3639550"
/tissue_type="Pancreas, adenocarcinoma"
/clone_lib="NIH MGC 39"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
137..595
/codon_start=1
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/protein_id="AAH04380.1"
/db_xref="GI:13325134"
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YVITGEVTVILFFILLYLRDLRMLKMLFPLDITNSLVTFMILVSLALIP
TTLTVGGGFALVTAVCCLDGALILYRKLLFNPSPGYOKRPHKEKVL"

CDS

201 a 138 c 154 g 195 t
BASE COUNT
ORIGIN

alignment_scores:

Quality: 471.50 Length: 152
Ratio: 4.763 Gaps: 1
Percent Similarity: 65.132 Percent Identity: 65.132

alignment_block:
US-09-801-115-2 x BC004380 ..

Align seg 1/1 to: BC004380 from: 1 to: 688

1 MetAspAnValGlnProIySIleIyShisARpGpocysPheSerVa 17
|||||
137 ATGGATACGTGACCGCGAAATAAACATCGCCCTTCTGCTAGGT 186
17 IlysgIyHISValIysmelleuArg..... 25
|||||
187 GAAAGCCACGCGAAGATGCTGCGCTGGCACTAAGTGCATCTANGA 236
25 25
237 CCTTTTATCATGCGACAGCCCTGAACATATATTGTATCATCTGA 286
25 25
287 TTGAAGTCACCGTTATCTATTTCATACTTTATATGACTCAGACT 336
26 LeuAspIleIleAsn 31
|||||
337 TGATGATTAATGAAGTGCTATTGTCCTTGTGCTATATATCAACT 386

31 erLeuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
|||||
387 CACTGTAACACACAGTATTCATGCTATGCTGTGTGGCACTGATA 436
48 ProGIuThrThrThrLeuThrValGlyGlyValAlaPheAlaLeuValTh 64
|||||
437 CCAGAAACCAACAAATTCAGTGTGAGGGGCTTGTGCACTGTGAC 486
64 rAlaValCysCysLeuAlaAspGlyAlaLeuIleIleYrArgIysLeuLeuP 81
|||||
487 AGCAGTATGCTGCTGTCCGACGCGGCCCTTATTACCGGAAGCTTCCT 536
81 heAsnProSerGlyProTyGlnLysLysProValHisGluIysGlu 97
537 TCAATCCACGCGCTCTACAGAAAAAACCTGTGATGAAAAAAGAA 586
98 ValLeu 99
|||||
587 GTTTTG 592

seq_name: gb_pr:AF135380

seq_documentation_block:

LOCUS AF135380 689 bp mRNA linear PRI 07-SEP-2000
DEFINITION Homo sapiens chemokine-like factor 2 (CKLF2) mRNA, complete cds,
alternatively spliced.
ACCESSION AF135380
VERSION AF135380.2 GI:9989692
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 689)
AUTHORS Han,W.L., Gu,W., Li,Y., Zhang,Y., Song,Q., Di,C. and Ma,D.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
2 (bases 1 to 689)
AUTHORS Han,W.L.
TITLE Direct Submission
JOURNAL Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China

REMARK Sequence update by submitter
COMMENT On Sep 7, 2000 this sequence version replaced gi:6630853.
FEATURES
location/Qualifiers
1..689
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/note="from PHA stimulated cells"
1..689
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/note="VCK"
148..606
/gene="CKLF2"
/note="VCK-2, alternatively spliced"
/codon_start=1
/product="Chemokine-like factor 2"
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/translation="MDNVQPKIKRPFCSYGVKMKRLALVTSMTFFITAOPEP
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BASE COUNT 195 a 140 c 161 g 193 t
ORIGIN

alignment_scores:

Quality: 471.50 Length: 152
Ratio: 4.763 Gaps: 1
Percent Similarity: 65.132 Percent Identity: 65.132

alignment_block:
US-09-801-115-2 x AF135380 ..

Align seg 1/1 to: AF135380 from: 1 to: 689

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1 MetaspasValGlnProLysIleLysHisArgProPheCysPheSerVa 17
  |||||||
148 ATGATTAACGTGCACGCCGAAATAAATACATGCCCTCTCTCTCAGTGT 197
17 ILysGlyHisValLysMetLeuArg..... 25
  |||||||
198 GAAAGGCCACGTGAAGATGCTGCAGCTGCACACTAAGTGTACATCTATGA 247
  |||||||
25 ..... 25
248 CTTTTTTATGATCGACACAGCCCTGAAACATATATTGTTATCAGTGA 297
  |||||||
25 ..... 25
298 TTGAGAGTCACCGTTATCTATTTTTCATCTTATATGCTACAGACT 347
  |||||||
26 ..... 31
348 TGATCGATTAAATGAAGTGTATTGTCCTTGTGCTGATATATCAACT 397
  |||||||
31 erLeuValThrThrValAlpheMetLeuIleValSerValLeuAlaLeuIle 47
  |||||||
398 CACGTGTACACACAGTATTCATGCTCATGCTATCTGTGTGGCACTGATA 447
  |||||||
48 ProGluThrThrThrLeuThrValGlyGlyValAlpheAlaLeuValTh 64
  |||||||
448 CCAGAAACACACACATTCACAGCTGTGTGAGGGGTGTGTGCACCTTGTCAC 497
  |||||||
64 rAlaValLysCysLeuAlaAspGlyAlaLeuIleThrArgLysLeuLeup 81
  |||||||
498 AGCACTATGCTGTCTTGGCGAGCGGCCCTTATTACCGAAGCTTCTGT 547
  |||||||
81 heAsnProSerGlyProTyrglnLysLysProValHisGlnLysLysL 97
  |||||||
548 TCATATCCAGCGGCTCTTACAGAAAAGCCTGTGCATGAAAAGAAAAA 597
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98 ValLeu 99
  |||||||
598 GTTTTG 603

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seq_name: gb_sts:G30204

seq_documentation_block:

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LOCUS      G30204                485 bp    DNA    linear    STS 05-OCT-1996
DEFINITION human STS SHGC-36487, sequence tagged site.
ACCESSION  G30204
VERSION    G30204.1 GI:1593755
KEYWORDS   STS; STS sequence; primer; sequence tagged site.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 485)
AUTHORS   Myers,R.M.
JOURNAL   Unpublished (1996)
COMMENT

```

Contact: Richard M. Myers
Stanford Human Genome Center (SHGC)
Stanford University School of Medicine
Department of Genetics, M-344, Stanford, CA 94305, USA
Tel: 4157259687
Fax: 4157259689
Email: myerseshgc.stanford.edu

Primer A: ACTTCTTTTTCATGACAGC
Primer B: GCCCTATTATCCGGAAGCT
STS size: 77
PCR profile:

Initial incubation: 94 degrees C for 90 seconds
Denaturation: 94 degrees C for 15 seconds
Annealing: 62 degrees C for 23 seconds
Polymerization: 72 degrees C for 30 seconds
PCR Cycles: 30
Thermal Cycler: Perkin Elmer 9600

Protocol:
Template: 25 ng
Primer: each 1 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uL
Total Vol: 10 uL

Buffer:
MgCl2: 2.5 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from T90569
-- Washington University/Merck EST sequence.

FEATURES
source 1..485
/organism="Homo sapiens"
/db_xref="taxon:9606"
/map="15"
STS
primer_bind 69..145
primer_bind 69..91
BASE COUNT 146 a 99 c 99 g 131 t 10 others
ORIGIN

alignment_scores:
Quality: 366.00 Length: 74
Ratio: 4.946 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 98.649

alignment_block:

US-09-801-115-2 x G30204/rev ..

Align seg 1/1 to reverse of: G30204 from: 1 to: 485

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26 LeuAspIleIleAsnSerLeuValThrThrValAlpheMetLeuIleValSe 42
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286 CTGATATATATCAACTCAGTGTACACAGTATTCATGCTCATCGTANC 237
  |||||||
42 rValLeuAlaLeuIleProGluThrThrThrLeuThrValGlyGlyL 59
  |||||||
236 TGTGTTGGCACTGATACAGAAACCAACACATTGACAGTGTGAGGGG 187
  |||||||
59 AlpheAlaLeuValThrAlaValLysCysLeuAlaAspGlyAlaLeuIle 75
  |||||||
186 TGTTCGACTTGTGACAGCAGTATGCTGTGCCGAGCGGCCCTTATT 137
  |||||||
76 TyrArgLysLeuLeuPheAsnProSerGlyProTyrglnLysLysProVA 92
  |||||||
136 TACCGAAGCTTCTGTCAATCCACAGCGGTCTTACAGAAAAGCGCTGT 87
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92 LHisGlnLysLysGlnValLeu 99
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86 GCATGAAAAAAGAGAGTTTG 65

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seq_name: gb_pr:AF145216

seq_documentation_block:

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LOCUS      AF145216                593 bp    mRNA    linear    PRI 07-SEP-2000
DEFINITION Homo sapiens chemokine-like factor 4 (CKLF4) mRNA, complete cds,
ACCESSION  AF145216
VERSION    AF145216.2 GI:9989694
KEYWORDS

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SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 593)
Han, W.L., Gu, W.F., Li, Y., Zhang, Y.M., Di, C.H., Song, Q.S. and Ma, D.L.
TITLE Direct Submission
JOURNAL Submitted (23-APR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
REFERENCE 2 (bases 1 to 593)
Han, W.L.
AUTHORS Direct Submission
JOURNAL Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK Sequence update by submitter
COMMENT On Sep 7, 2000 this sequence version replaced gi:6625671.
FEATURES
location/Qualifiers
1..593
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/note="from PHA stimulated cells"
1..593
/gene="CKLF4"
/note="UCK"
148..510
/gene="CKLF4"
/note="UCK-4: alternatively spliced"
/codon_start=1
/product="chemokine-like factor 4"
/protein_id="AAFI9350.1"
/db_xref="GI:6625672"
/translation="MDNVOPKIKHRPFCFSVKGHVKMLRLVFTVSMTEFIITAOAPE
YIVTVEFVTLFFILYVLRLDRLMKLPLVFLVAVVCLADGALIRKLLF
NPSGYOKRPVHEKEVLT"
BASE COUNT 166 a 120 c 140 g 167 t
ORIGIN

alignment_scores:
Quality: 339.50 Length: 126
Ratio: 4.297 Gaps: 2
Percent Similarity: 62.698 Percent Identity: 57.937

alignment_block:
US-09-801-115-2 x AFI45216 ..
Align seg 1/1 to: AFI45216 from: 1 to: 593

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1 MetaspasnaValGlnProLysIleLysHisArgProPhocysPheSerVa 17
|||||
148 ATGATTAACGTCGACGCGAATAAATGCGCCCTTCGCTTCACTGT 197
17 llysglyHisValysMetLeuArgLeuAspIleIleAsnSerLeuValT 34
|||||
198 GAAAGGCCACGTCGAAGATGCTGCGCTGCACATTA..... 231
34 hrThrValPheMetLeuIleValSerValLeuAlaLeuIleProGlnThr 50
|||||
232 ..ACTGTGACATCTTATGACCTTTTATTCATCGACCAAGCCCTGAACCA 279
51 ThrThrLeuThrValGlyGlyGly..... 58
:::
280 TATATTTGTTATCACTGATTTGAAGTCACCGTTATCTATTTCATCT 329
58 .....
330 TTTATATCTACTCAGACTGATCGATTATGAAGTGTATTGCGCTT 379
59 .....ValPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAla 73
|||||
380 TCGTTGTGTGACCTGTGACGACGATGCTGTCTTGTCCGACGAGGCC 429

```

74 LeuIleTyArgLysLeuLeuPheAsnProSerGlyProTyGlnLysTy 90
|||||
430 CTTATTATACCGAAGCTTCTGTTCAATCCACGCGGCTTTCACAGAAAA 479
90 sProValHisGluLysLysGluValLeu 99
|||||
480 GCCTGTGTCATGAAAAAAGAAAGTTTGG 507
seq_name: gb_pr:AF135381
seq_documentation_block:
LOCUS AFI35381 434 bp mRNA linear PRI 07-SEP-2000
DEFINITION Homo sapiens chemokine-like factor 3 (CKLF3) mRNA, complete cds,
alternatively spliced.
ACCESSION AFI35381
VERSION AFI35381.2 GI:9989693
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Mammalia: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS 1 (bases 1 to 434)
Han, W.L., Gu, W.F., Li, Y., Zhang, Y., Song, Q., Di, C. and Ma, D.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue
Yuan Road, Beijing 100083, China
REFERENCE 2 (bases 1 to 434)
Han, W.L.
AUTHORS Direct Submission
JOURNAL Submitted (07-SEP-2000) Immunology, Peking University Health
Science Center, Xueyuan Road 38, Beijing 100083, China
REMARK Sequence update by submitter
COMMENT On Sep 7, 2000 this sequence version replaced gi:6630855.
FEATURES
location/Qualifiers
1..434
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="U937"
/note="from PHA stimulated cells"
1..434
/gene="CKLF3"
/note="UCK"
148..351
/gene="CKLF3"
/note="UCK-3: alternatively spliced"
/codon_start=1
/product="chemokine-like factor 3"
/protein_id="AAFI9600.1"
/db_xref="GI:6630856"
/translation="MDNVOPKIKHRPFCFSVKGHVKMLRLVFLVAVVCLADGALIT
RKLLFNNGGYOKRPVHEKEVLT"
BASE COUNT 127 a 88 c 116 g 103 t
ORIGIN

alignment_scores:
Quality: 331.00 Length: 99
Ratio: 4.940 Gaps: 1
Percent Similarity: 67.677 Percent Identity: 67.677

alignment_block:
US-09-801-115-2 x AFI35381 ..
Align seg 1/1 to: AFI35381 from: 1 to: 434

```

1 MetaspasnaValGlnProLysIleLysHisArgProPhocysPheSerVa 17
|||||
148 ATGATTAACGTCGACGCGAATAAATGCGCCCTTCGCTTCACTGT 197
17 llysglyHisValysMetLeuArgLeuAspIleIleAsnSerLeuValT 34
|||||
198 GAAAGGCCACGTCGAAGATGCTGCGCTGCACATTA..... 225

```

```

34 hThrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
225 .....
51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCy 67
226 .....GTGTTGCACCTGTGACAGCAGTATG 251
67 scysLeuAlaaspGlyAlaLeuIleIleYrArgLysLeuLeuPheAspPro 84
252 CTGTCTTGGCCGAGGGGCCCTTATTATTCGGAAGCTTGTTGTAATCCCA 301
84 ergLysProTyrGlnLysLysProValHisGluLysLysGluValLeu 99
302 GGGGTCCTTACCAGAAAGGCTGTGTCATGAAAAAGAGATTG 348
seq_name: gb_pat:AX079435

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LOCUS	AX079435	495 bp	DNA	linear	PAT 22-FEB-2001
DEFINITION	Sequence 179 from Patent WO0107611.				
ACCESSION	AX079435				
VERSION	AX079435.1	GI:13158995			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
REFERENCE	1 (bases 1 to 495)				
AUTHORS	Baker,K.P., Goddard,A. and Wood,W.I.				
TITLE	Human polypeptides and methods for the use thereof				
JOURNAL	Patent: WO 0107611-A 179 01-FEB-2001; Genentech, Inc. (US)				
FEATURES	location/Qualifiers				
source	1..495				
	/organism="Homo sapiens"				
	/db_xref="taxon:9606				
BASE COUNT	119 a	103 c	127 g	142 t	4 others
ORIGIN					

alignment_scores:	
Quality:	318.50
Ratio:	4.550
Percent Similarity:	56.452
	Percent Identity: 56.452

alignment_block:
US-09-801-115-2 x AX079435

Align seg 1/1 to: AX079435 from: 1 to: 495

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1  MetaspasVallInProlysIleLysHisIaArgProPheCysPheSerVa 17
124  ATGGATACCTGCAGCCGAAANNTAAACATGCCCCCTTCTGCTCAGTGT 17
17  LysGlyHisValLysMetLeuArg 17
174  GAAAGGCCACGTTGAAGATGCTGCGGTGCACCTAACTGACATCTATGA 22
25  ..... 25
224  CCTTTTATNATGCGACACGCCCTGAAACCTATATTTGATCATCTGGA 27
25  ..... 25
274  TTGGAAGTCACCGTTATCTTATTTTCATACCTTTATATGACTCAGACT 32
26  ..... LeuAspIleIleAsn 31
324  TGATCGATTATGAAGTGGTTATTTTGGCCCTTGGTTGATATATCAACT 37
31  erLeuValThrThrValLpMetMetLeuIleValSerValLeuAlaLeuIle 47

```

374 CACTGTACACAAAGATTATCATGCTCATCGATCTGTTGGACATATA 423
48 ProGluThrThrIleuThrAlaGlyAlaGlyValAlaPheAlaLeuValTh 64
424 CCAGAAACCAACAATGTCACAGTGGTGGAGGGGTGTGGACATTGGAC 473
64 rAlaValCysCysLeuAlaASP 71
474 AGCAGTATGCTGTGTTNTGGCCGAC 455

seq_name: gjb_ro:AF253064

LOCUS	AF253064	523 bp	mRNA	linear	ROD 27-NOV-2001
DEFINITION	<i>Rattus norvegicus</i> chemokine-like factor 1 (CXCL1) mRNA, complete cds.				
ACCESSION	AF253064				
VERSION	AF253064.2	GI:17105378			
KEYWORDS					
SOURCE	Norway rat.				
ORGANISM	<i>Rattus norvegicus</i>				

REFERENCE 1 (bases 1 to 523)

AUTHORS Sou, Y., Li, Y., Han, W., Song, Q., Zhang, Y., Di, C. and Ma, D.
TITLE Direct Submersion
JOURNAL Submitted (06-APR-2000) Immunology, Beijing Medical University
Xueyuan Road, Beijing 100083, China

REFERENCE 2 (phases 1 to 523)
AUTHORS Lou, Y., Li, Y., Han, W., Song, Q., Zhang, Y., Di, C. and Ma, D.
TITLE Direct Submission
JOURNAL Submitted (27-NOV-2001) Immunology, Beijing Medical University
Xueyuan Road, Beijing 100083, China

REMARK	Sequence update by submitter
COMMENT	On Nov 27, 2001 this sequence version replaced gl:7769680
FEATURES	Location/Qualifiers

source

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/organism="Rattus norvegicus"
/strain="Wistar"
/db_xref="taxon:10116"
/tissue_type="liver"
1..523
/gene="CKLF1"
167..463

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/ gene ...
/ note="cyt
/codon_sta

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/product=chemokine line id
/protein_id="AAF69502.1"
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BASE COUNT	ORIGIN	134 a	107 c	133 g	149 t
/translation="MDSFQKVVNDHQPECLSKCVKTLRLDYINSVTTFLMLIVSY					
ALIPETSTMWGVGFLEFLVICVACACALMCQRLRPRGPQYNRSATDVDS"					

alignment_scores:

Quality:	275.00	Length:	90
Ratio:	3.667	Gaps:	0
Percent Similarity:	83.333	Percent Identity:	58.889

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alignment_block:
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Align seg 1/1 to: AF253064 from: 1 to: 523

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1  MetAspAsnValAlaGlnProLysIleLysHisArgProPheCysPheSerVal 17
      |||||::: ||| :::: |||||:::|||||:::|||||:::
167 ATGGACTCTCCACACAGAGAGTCTGTAGACCATATGAGCCCTTTCTCCCACTCT 216
      |||||:::|||||:::|||||:::|||||:::|||||:::
17  LysGlyHisValLysMetLeuArgLeuAspIleLeuLeuSerLeuValT 34

```



```

217 GAATGCTTTGTGAAGCGCTGGATGTTATCACTCGGTGTAA 266
34 hTrrValPheMetLeuIleValSerValLeuAlaLeuIleProGluThr 50
267 CAACACATTCATCGTATGTTGTCTGCGGTCTTAATACAGAAAC 316
51 ThrThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValC 67
317 TCAACATGATTAATGTTGGAGGGGTCTTGGTTCTTGACAGTAATATG 366
67 sCysLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnPro 84
367 TACTGTGCTGATGTGCTTATGTCAGAAACCTCGGTTTCGTCAC 416
84 ergLysProTyrGlnLysLys 90
417 ATGGAACCTTATCAGACAGG 436
seq_name: gb_pat:AX330610

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```

seq_documentation_block:
LOCUS AX330610 207 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 1119 from Patent WO0194629.
ACCESSION AX330610
VERSION AX330610.1 GI:18103588
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (sites)
Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horriagan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
TITLE
gene sets
JOURNAL Patent: WO 0194629-A 1119 13-DEC-2001;
FEATURES
source 1. 207
location/Qualifiers
BASE COUNT 70 a 43 c 39 g 54 t 1 others
ORIGIN

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alignment_scores:
Quality: 245.00 Length: 48
Ratio: 5.213 Gaps: 0
Percent Similarity: 97.917 Percent Identity: 97.917

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alignment_block:
US-09-801-115-2 x AX330610/rev ..

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Align seg 1/1 to reverse of: AX330610 from: 1 to: 207

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52 ThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCysC 68
|||||
205 ACATTGACAGTTGGTGGAGGGGTCTTGCACTTGACAGAGTAATCTG 156
68 sLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSer 85
|||||
155 TCTTGGCCGAGCGGCCCTTATTATCCGGAAGCTTCTGTCATATCCAGCG 106
85 LysProTyrGlnLysLysProValHisGlnLysLysGlnValLeu 99
|||||
105 GTCTTACCAAGNAAAAGCCTGTGATGAAAAAAGAAAGTTTG 62
seq_name: gb_pat:AX330787

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seq_documentation_block:
LOCUS AX330787 207 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 1296 from Patent WO0194629.

```

```

ACCESSION AX330787
VERSION AX330787.1 GI:18103765
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (sites)
Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horriagan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
TITLE
gene sets
JOURNAL Patent: WO 0194629-A 1296 13-DEC-2001;
FEATURES
source 1. 207
location/Qualifiers
BASE COUNT 70 a 43 c 39 g 54 t 1 others
ORIGIN

```

```

alignment_scores:
Quality: 245.00 Length: 48
Ratio: 5.213 Gaps: 0
Percent Similarity: 97.917 Percent Identity: 97.917

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alignment_block:
US-09-801-115-2 x AX330787/rev ..

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```

Align seg 1/1 to reverse of: AX330787 from: 1 to: 207

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52 ThrLeuThrValGlyGlyValPheAlaLeuValThrAlaValCysC 68
|||||
205 ACATTGACAGTTGGTGGAGGGGTCTTGCACTTGACAGAGTAATCTG 156
68 sLeuAlaAspGlyAlaLeuIleTyrArgLysLeuLeuPheAsnProSer 85
|||||
155 TCTTGGCCGAGCGGCCCTTATTATCCGGAAGCTTCTGTCATATCCAGCG 106
85 LysProTyrGlnLysLysProValHisGlnLysLysGlnValLeu 99
|||||
105 GTCTTACCAAGNAAAAGCCTGTGATGAAAAAAGAAAGTTTG 62
seq_name: gb_pat:AX331008

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seq_documentation_block:
LOCUS AX331008 207 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 1517 from Patent WO0194629.
ACCESSION AX331008
VERSION AX331008.1 GI:18121642
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (sites)
Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horriagan,S., Soppet,D.R. and Weaver,Z.
Cancer gene determination and therapeutic screening using signature
TITLE
gene sets
JOURNAL Patent: WO 0194629-A 1517 13-DEC-2001;
FEATURES
source 1. 207
location/Qualifiers
BASE COUNT 70 a 43 c 39 g 54 t 1 others
ORIGIN

```

```

alignment_scores:
Quality: 245.00 Length: 48

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Ratio: 5.213 Gaps: 0
Percent Similarity: 97.917 Percent Identity: 97.917

alignment_block:

US-09-801-115-2 x AX331008/rev ..

Align seg 1/1 to reverse of: AX331008 from: 1 to: 207

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52 ThrleuThrValGlyGlyValAlaPheAlaLeuValThrAlaValCysCy 68
|||||
205 ACATTGACAGTGTGTGGAGGGGTGTTGCACTGTGTGACAGCAGATGCTG 156
|||||
68 sleuAlaAspGlyAlaLeuIleTyArgLysLeuLeuPheAsnProSerG 85
|||||
155 TCTTGCCGACGCGGCCCTTATTATTCGGAAGCTTGTGTCAATCCCGCGC 106
|||||
85 lYProTyGlnLysLysProValHisGlnLysLysGlnValLeu 99
|||||
105 GTCCTTACAGNMAAGCTGTGCATGAAAAAAGAGATTTC 62
```

seq_name: gb_to:AF253065

seq_documentation_block:

LOCUS AF253065 682 bp mRNA linear ROD 27-NOV-2001
DEFINITION Rattus norvegicus chemokine-like factor 2 (CKLF2) mRNA, complete

ACCESSION AF253065
VERSION AF253065.2 GI:17105379

KEYWORDS

SOURCE Norway rat.
ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

REFERENCE

1 (bases 1 to 682)
Lou, Y., Li, Y., Han, W., Song, Q., Zhang, Y., Di, C. and Ma, D.

JOURNAL Submitted (06-APR-2000) Immunology, Beijing Medical University,
Xueyuan Road, Beijing 100083, China

2 (bases 1 to 682)
Lou, Y., Li, Y., Han, W., Song, Q., Zhang, Y., Di, C. and Ma, D.

JOURNAL Direct Submission
Submitted (27-NOV-2001) Immunology, Beijing Medical University,
Xueyuan Road, Beijing 100083, China

REMARK COMMENT
Sequence update by submitter
On Nov 27, 2001 this sequence version replaced gi:7769682.

FEATURES
Location/Qualifiers

1..682
/organism="Rattus norvegicus"
/strain="Wistar"

/db_xref="taxon:10116"
/tissue_type="liver"

1..682
/gene="CKLF2"

167..622
/gene="CKLF2"

/note="cytokine: similar to Homo sapiens CKLF2"
/codon_start=1
/product="chemokine-like factor 2"

/protein_id="AAF69503.1"
/db_xref="GI:7769683"

/translation="MDSPOKVVYDHPFCLSLKCFYKTLRLVYTVASMTFFVAQAP
YIVTGFERTITLFLALMCSLDKTRSFEMFLDVINSVVTILFMLIVSALIP
TSTMVGVGVFGLVICTVADCALMCQKLRFRPHGPYQNRSATDVDS"

BASE COUNT 167 a 143 c 163 g 209 t

ORIGIN

alignment_scores:
Quality: 238.50 Length: 143
Ratio: 3.180 Gaps: 1
Percent Similarity: 52.448 Percent Identity: 37.063

alignment_block:
US-09-801-115-2 x AF253065 ..

Align seg 1/1 to: AF253065 from: 1 to: 682

```
1 MetAspAsnValGlnProLysIleLysHisArgProPheCysPheSerVal 17
|||||
167 ATGACTCTCCACAGAGAGTGTGAGACATCAGCCCTTGTGCTCAGTCT 216
|||||
17 LysGlnHisValLysMetLeuArg..... 25
|||||
217 GAAATGCTTTGTGAAGACCTGGGTTGGTGTGAACGTGGGCTGTANGA 266
|||||
25 ..... 25
267 TCTTTTCATTGTGGCACAAGCCCTGAACCGTATATGTCATCACTGGG 316
|||||
25 ..... 25
317 TTGGAAGTCAACCATCTCTCTTCTCATAGCCTTATATATGTCAGTCT 366
|||||
26 ..... LeuAspIleIleAsnS 31
|||||
367 TGACAAGACAAGAGATCTTCTTTGGCCTTGTGATGTATCACTACT 416
|||||
31 erleuValThrThrValPheMetLeuIleValSerValLeuAlaLeuIle 47
|||||
417 CGGTGTGTACACACATCATCTATGTGTGTGTGTGTGTGTGTGTGTATA 466
|||||
48 ProGlnThrThrThrThrValGlyGlyValAlaPheAlaLeuValrh 64
|||||
467 CCGAAGACCTCAACAAATGATATAGTTGGAGGGGTGTGGTTGCTCTGAC 516
|||||
64 lAlaValCysCysLeuAlaAspGlyAlaLeuIleTyArgLysLeuLeuP 81
|||||
517 AGAATATATGACGTGTGATGTGTGCTTATGTGTCAGCAAGAACGCGGT 566
|||||
81 heAsnProSerGlyProTyGlnLysLys 90
|||||
567 TTGCTCCACATGACCTTATCAGAACAGG 595
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